

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2002, 16:28:59 ; Search time 1539.98 seconds

(Without alignments)
22389.320 Million cell updates/sec

Title: US-09-636-826-1

Perfect score: 2090

Sequence: 1 GATATCACACATTCGTTCAT.....TCGCTTCTCGGTCTGCT

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1472140 seqs, 8248589755 residues

Word size: 0

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seg length: 0

Maximum DB seg length: 2000000000

Post-processing: listing first 45 summaries

Database:

GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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13: gb_un:*
14: gb_vi:*
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31: em_hgtg_inv:*
32: em_hgtg_rnd:*
33: em_hgtg_hum:*
34: em_hgtg_inv:*
35: em_hgtg_rnd:*
36: em_hgtg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2090	100.0	2090	6	AX088250	AX088250 Sequence
2	29	1.4	991	8	MCVTRPC	X9499 M.Crystalli
3	26	1.2	13862	3	CEP39B1	269660 Caenorhabdi
4	25	1.2	86156	9	HUAC002550	AC002550 Human Chr
5	25	1.2	166116	2	AL360221	AL360221 Homo sapi
6	25	1.2	184666	2	AC013508	AC013508 Homo sapi
7	25	1.2	188120	2	AC032169	AL392169 Homo sapi
8	25	1.2	193305	2	AC093278	AC093278 Homo sapi
9	25	1.2	199517	9	AL353741	AL353741 Human DNA
10	25	1.2	211271	2	AL590624	AL590624 Homo sapi
11	24	1.1	1366	3	PFGBPH21	X69769 P.Falciptaru
12	24	1.1	1366	3	PFGBPH21	X79836 P.Falciptaru
13	24	1.1	8077	2	AC019982	AC019982 Drosophila
14	24	1.1	107257	10	AF289665	AF289665 Mus muscu
15	24	1.1	114898	10	AF139987	AF139987 Mus muscu
16	24	1.1	123004	2	AC014962	AC014962 Drosophila
17	24	1.1	148744	9	AL355576	AL355576 Human DNA
18	24	1.1	175561	9	AC012636	AC012636 Homo sapi
19	24	1.1	177129	2	AC037481	AC037481 Homo sapi
20	24	1.1	179947	2	AC009786	AC009786 Homo sapi
21	24	1.1	192581	2	PFMAL13P1	AL049180 Plasmodiu
22	24	1.1	194188	2	AC044857	AC044857 Homo sapi
23	24	1.1	200849	2	AC091250	AC091250 Mus muscu
24	24	1.1	224843	2	AC021223	AC021223 Homo sapi
25	24	1.1	289887	3	AE003542	AE003542 Drosophila
26	24	1.1	300503	2	AC010260	AC010260 Homo sapi
27	24	1.1	305018	3	AE003437	AE003437 Drosophila
28	23	1.1	1208	5	AF123885	AF123885 Gallus ga
29	23	1.1	38192	2	AC020177	AC020177 Drosophila
30	23	1.1	61756	2	AC017569	AC017569 Drosophila
31	23	1.1	75762	2	AC036137	AC036137 Homo sapi
32	23	1.1	77585	9	AL133418	AL133418 Human DNA
33	23	1.1	77635	2	DMBR40C10	AL122024 Drosophila
34	23	1.1	90157	9	AL355552	AL355552 Human DNA
35	23	1.1	103675	2	HSDJ93P18	AP080251 Homo sapi
36	23	1.1	113733	2	AP003159	AP003159 Homo sapi
37	23	1.1	11674	2	DMBR30C13	AL122025 Drosophila
38	23	1.1	130494	2	AL139422	AL139422 Homo sapi
39	23	1.1	133221	9	HS339A15	AL031423 Human DNA
40	23	1.1	141184	2	AL139283	AL139283 Homo sapi
41	23	1.1	144260	9	AC006998	AC006998 Homo sapi
42	23	1.1	146516	2	AC079981	AC079981 Homo sapi
43	23	1.1	148430	9	AL139328	AL139328 Human DNA
44	23	1.1	153724	2	AC041034	AC041034 Homo sapi
45	23	1.1	154935	2	AL356781	AL356781 Homo sapi

ALIGNMENTS

RESULT	1	LOCUS	AX088250	2090 bp	DNA	PAT	17-MAR-2001
DEFINITION	Sequence 1 from Patent WO0114572.						
ACCESSION	AX088250						
VERSION	AX088250.1	GI:13397159					
KEYWORDS							
SOURCE	Beta vulgaris.						
ORGANISM	Beta vulgaris						
REFERENCE	Duveny E. and Rausch, T.						
AUTHORS							
TITLE	Plant gene expression, controlled by constitutive plant v-atpase promoters						
JOURNAL	Patent: WO 0114572-A 1 01-MAR-2001;						
FEATURES	BASE ANTISENSE/SHAFT (DE)						
source	Location/Qualifiers						
	1..2090						

/organism="Beta vulgaris"
/db_xref="taxon:161934"
/note="Promotor subunit c isoform 2"
1..1923
BASE COUNT 794 a 354 c 271 g 671 t
ORIGIN

Query Match 100.0%; Score 2090; DB 6; Length 2090;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2090; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 1 GATATGACACATTCGTCATCGACGATTTGGCACTTCAAAAGCTAGCTATTTCTTTT 60
DB 1 GATATGACACATTCGTCATCGACGATTTGGCACTTCAAAAGCTAGCTATTTCTTTT 60
OY 61 AATCTTCAAGTATTTGACATTTGACATTTGACATTTGACATTTGACATTTGACATTT 120
DB 61 AATCTTCAAGTATTTGACATTTGACATTTGACATTTGACATTTGACATTTGACATTT 120
OY 121 GGAATTAAGTGAAGGGGTGTTATATATATAGACTTAAATTTGATTCATTTTCAATAT 180
DB 121 GGAATTAAGTGAAGGGGTGTTATATATATAGACTTAAATTTGATTCATTTTCAATAT 180
OY 181 CTGAAGACAGGATGATGTAATTTGATTCATTTGATTCATTTGATTCATTTGATTCAT 240
DB 181 CTGAAGACAGGATGATGTAATTTGATTCATTTGATTCATTTGATTCATTTGATTCAT 240
OY 241 TTTAGTCTTTTAAAAATTCATATATATATTTTGGCCAAACCTTTGCAAAATATC 300
DB 241 TTTAGTCTTTTAAAAATTCATATATATATTTTGGCCAAACCTTTGCAAAATATC 300
OY 301 CATGTGCGAAATATTTGAAAAACCAATATCAACCTTTTGGCAACACTTT 360
DB 301 CATGTGCGAAATATTTGAAAAACCAATATCAACCTTTTGGCAACACTTT 360
OY 361 TACAAAAATCCATTTTCAGAAAAAAATTTTACATTTTACCTTTGCAAAATCAAAATG 420
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OY 421 GAAAAATTTAAATTTGCTTTCACCTATATATGAAAGTGAAGTGAAGTGAAGTGAAG 480
DB 421 GAAAAATTTAAATTTGCTTTCACCTATATATGAAAGTGAAGTGAAGTGAAGTGAAG 480
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DB 481 GGAGAAAAATAAAAATGACATTTTCATGCAAAATCAAAATGCTATGAAAACTTAAAA 540
OY 541 TTTTATTTTAAATATATGAAATCAAGTGTAAATTTAGAAAAAGGAAAAATTA 600
DB 541 TTTTATTTTAAATATATGAAATCAAGTGTAAATTTAGAAAAAGGAAAAATTA 600
OY 601 AATGACATTTTCATTCAAATCAGATTTGTATGAAAAATTTAAATTTTATTTCAATA 660
DB 601 AATGACATTTTCATTCAAATCAGATTTGTATGAAAAATTTAAATTTTATTTCAATA 660
OY 661 TAATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
DB 661 TAATGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720
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DB 901 GTAAAGACATCATCTGATTTATTAAGAACATGCGCATTTAGAAATGAGAAAAA 960
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OY 1021 CAAATGAGAGTGAATTTAAATTTACTTATTTGATTTGATTTGATTTGATTTGATTT 1080
DB 1021 CAAATGAGAGTGAATTTAAATTTACTTATTTGATTTGATTTGATTTGATTTGATTT 1080
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DB 1141 GTCAAAACATCAACATGATTTTCAATTTAGCTTCAATTTGATTTGATTTGATTTGAT 1200
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DB 1261 AACGTTTCCCTTGGGGTAAATTTACTTCCAAATGATGAAACCATTTTCTTCAA 1320
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DB 1381 TTTCCCTTTTATTTTACTTTCATTTCAATTTTCTTGGATGAAACCAACAGGAA 1440
OY 1441 ACTATTTTGAATTTGTTTCCATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1500
DB 1441 ACTATTTTGAATTTGTTTCCATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 1500
OY 1501 GAAAAATTTTACACCTTACCAACAGAGGCTGTTGTCATGAAATGATGACGATTT 1560
DB 1501 GAAAAATTTTACACCTTACCAACAGAGGCTGTTGTCATGAAATGATGACGATTT 1560
OY 1561 CAATTCGAACCTGTTTACCTTCCATTTGATTTGATTTGATTTGATTTGATTTGATTT 1620
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OY 1801 CTCCCAATTTTCAATTTTATTTATTCAGGGGAAATGATCAAAATTTCAATTTCA 1860
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OY 1861 AAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
DB 1861 AAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
OY 1921 CTCATATTTCAATTCACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
DB 1921 CTCATATTTCAATTCACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
OY 1981 TCGGATCAAGCATTCATGACACCTTCCGATATATACCATGAAAAAATGCAACG 2040
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Db 1981 TCGATCAGCAATTCATCGACACCTTCGATCATCACCATCAAAAAATGTCAACAG 2040
OY 2041 TCTTAAGGGGATGAACGGCCGCTTCGCTTCGGGCTGCT 2090
Db 2041 TCTTAAGGGGATGAACGGCCGCTTCGCTTCGGGCTGCT 2090

RESULT 2
MCVATPC 991 bp mRNA PLN 21-OCT-1996
LOCUS M.crystallinum mRNA for v-type ATPase c subunit.
ACCESSION X84999
VERSION X84999.1 GI:1495682
KEYWORDS ATPase c subunit.
SOURCE common ice plant.
ORGANISM Mesembryanthemum crystallinum
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Caryophyllales; Caryophyllales; Alzooceae; Mesembryanthemum.
REFERENCE
AUTHORS Tsiantis/M.S., Bartholomew/D.M. and Smith,J.A.
TITLE Salt regulation of transcript levels for the c subunit of a leaf
vacuolar H(+) -ATPase in the halophyte Mesembryanthemum crystallinum
MEDLINE 96337458
REFERENCE 2 (bases 1 to 991)
AUTHORS Tsiantis/M.S.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-1996) M.S. Tsiantis, Dept. of Plant Sciences,
University of Oxford, South Parks Rd., Oxford, OX1 3RB, UK

FEATURES
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1..991
location/Qualifiers
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115..612
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115..612
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/db_xref="GI:1495683"
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GIAGISGMAIGIVGDAGVANAQPKLVGMILITIPRALALVGLIVGITLSRAS
OSRAD"
864..869
polyA_signal
973..978
polyA_signal
BASE COUNT 195 a 216 c 220 g 360 t
ORIGIN

Query Match 1.44: Score 29: DB 8: Length 991:
Best Local Similarity 100.0%; Pred.No.0.026;
Matches 29: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2049 GAGCATGAACGGCCGCTTCGCTTCGGGCT 2077
Db 133 GAGCATGAACGGCCGCTTCGCTTCGGGCT 161

RESULT 3
CEF39B1 13862 bp DNA INV 25-OCT-2000
LOCUS Caenorhabditis elegans cosmid F39B1, complete sequence.
DEFINITION Z69660
ACCESSION Z69660.1 GI:1200273
VERSION Z69660.1
KEYWORDS H1e; Phosphatidylinositol 3-kinase like; Transfer RNA; tRNA-val.
SOURCE Caenorhabditis elegans.
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;

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REFERENCE
AUTHORS none.
TITLE 1 (bases 1 to 13862)
JOURNAL Genome sequence of the nematode C. elegans: a platform for
MEDLINE investigating biology. The C. elegans Sequencing Consortium
REMARK Science 282 (5396), 2012-2018 (1998)
99069613
The C.elegans Sequencing Consortium.
Erratum: [[published errata appear in Science 1999 Jan
1:283(5398):35 and 1999 Mar 26:283(5410):2103 and 1999 Sep
3:283(5433):1493]]
2 (bases 1 to 13862)
Lightning,J.
REFERENCE
AUTHORS Direct Submission
TITLE Submitted (24-FEB-1996) Nematode Sequencing Project, Sanger Centre,
JOURNAL Hinxton, Cambridge CB10 1RQ, England and Department of Genetics,
Washington University, St. Louis, MO 63110, USA. E-mail:
jassanger.ac.uk or twenematode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from GeneFINDER (P. Green, U. Washington), and other
available information.
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is not the entire insert of clone F39B1.
It may be shorter because we only sequence overlapping sections
once, or longer because we arrange for a small overlap between
neighbouring submissions.
The true left end of clone F39B1 is at 1 in this sequence. The true
right end of clone F39B1 is at 21038 in
sequence Z69903.
The true left end of clone F4672 is at 13764 in this sequence. The
start of this sequence (1..100) overlaps with the end of sequence
Z93239.
The end of this sequence (13764..13862) overlaps with the start of
sequence Z69903.
For a graphical representation of this sequence and its analysis
see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
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location/Qualifiers
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/db_xref="taxon:6239"
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complement(269903.1:2880..3094),
complement(269903.1:1891..1999),
complement(269903.1:1618..1846),
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complement(269903.1:4079..4228),
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complement(7166..7311),complement(6892..7089))

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[illegible]

FEATURES
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/clone="A-101F10"
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/gene="101F10.2"
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/db_xref="GI:2911265"
/translation="MINIDGKKRPSFLEFLCNFFSLIIVDPHPEGVLEFVREL LNVIDYTWEDNSDEKIRIYTCVHLISAMSGEYLIHDKVDSNDISYGGDSKFLAE NKKLCETVAQILIEHLTKAKDEALRKSSGLSPFNLSIAGSDLRNKKMLQSLVNLW HLAQRGSCADIRKMYTLEIRYIKKQSKQPMHTLTELALRLPLQTRT"
BASE COUNT 23581 a 19688 c 20974 g 21913 t
ORIGIN

Query Match 1.2%: Score 25; DB 9; Length 86156;
Best Local Similarity 100.0%: Pred No. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1859 AAAAAAAAAATAAATAAAGAGAAAG 1883
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Db 51552 AAAAAAAAAATAAATAAAGAGAAAG 51576
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RESULT 5
AL360221 166116 bp DNA HTG 16-MAY-2001
LOCUS Homo sapiens chromosome 9 clone RP11-279E1, *** SEQUENCING IN
DEFINITION
PROGRESS ***, 4 unordered pieces.
ACCESSION AL360221

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AL360221.11 GI:13157574
HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLPROP.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euteria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 166116)
Skuce, C.
Direct Submission
Submitted (15-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humgery@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Feb 27, 2001 this sequence version replaced gi:13092300.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humgery@sanger.ac.uk
----- Project Information
Center project name: b279E1
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-termination Big Dye; 100% of reads
Consensus quality: 164733 bases at least Q40
Consensus quality: 165336 bases at least Q30
Consensus quality: 165816; sum-of-coverage
Insert size: 158936; 8.7% error; agarose-fp
Quality coverage: 6.79x in Q20 bases; sum-of-coverage
coverage: 7.13x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 34340: contig of 34340 bp in length
* 34341 34440: gap of 100 bp
* 34441 100244: contig of 65804 bp in length
* 100245 100344: gap of 100 bp
* 100345 123592: contig of 23248 bp in length
* 123593 123692: gap of 100 bp
* 123693 166116: contig of 42424 bp in length.
Location/Qualifiers
1. 166116
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-279E1"
/clone_1lb="RP11-11.1"
1. 34340
/note="assembly-fragment:02226
vector:side:left"
clone_end:sp6
vector:side:right"
34441. 100244
/note="assembly-fragment:01386
fragment_chain:1"
100345. 123592
/note="assembly-fragment:02487
fragment_chain:1"
123693. 166116
/note="assembly-fragment:01891
clone_end:tt7
vector:side:right"
BASE COUNT 50579 a 32344 c 31958 g 50934 t 301 others
ORIGIN

Query Match 1.2%: Score 25; DB 2; Length 166116;

Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1859 AAAAAAAAAATATAAGAAAG 1883
Db 157781 AAAAAAAAAATATAAGAAAG 157757

RESULT 6
AC013508 184666 bp DNA HTG 09-SEP-2000
LOCUS Homo sapiens clone RP11-11516, WORKING DRAFT SEQUENCE, 20 unordered
DEFINITION pieces.
AC013508
AC013508.3 GI:10045243
VERSION HTG: HTGS_PHAS1; HTGS_DRAFT.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM

REFERENCE
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
TITLE 1 (bases 1 to 184666)
JOURNAL Homo sapiens, clone RP11-11516
REFERENCE
AUTHORS 2 (bases 1 to 184666)
REFERENCE
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barlow, N., Beckel, R., Boguski, L., Bouckert, B.,
Brown, A., Castle, A., Collins, S., Collins, S., Collins, A.,
Cooke, P., Dearlano, K., Dewar, K., Dominko, M., Donnelly, P.,
Fitzgerald, P., Fitzhugh, M., Forrest, C., Funke, R., Gage, D.,
Gallardo, J., Gardiner, S., Grant, G., Haggis, B., Heath, A., Horton, L.,
Howland, J., Johnson, R., Jones, C., Kapp, L., Karas, A., Klein, J.,
Lehoczky, J., Lien, C., Locke, K., MacDonald, P., Marquis, N.,
McEwen, P., McGuire, A., McKernan, K., McLaughlin, J., Meldrum, T.,
Morrow, D., Naylor, J., Norman, C., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tasfai, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wymann, D., Ye, W., Zimmer, A. and Zody, M.

TITLE
JOURNAL Direct Submission
COMMENT Submitted (13-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA.
On Sep 9, 2000 this sequence version replaced gi:6479139.
All repeats were identified using RepeatMasker:
Smith, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: L1876
Center clone name: 115.1-6
Summary Statistics
Sequencing vector: M13, M77815, 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Assembly program: Phrap, version 0.960731
Consensus quality: 159232 bases at least Q40
Consensus quality: 174889 bases at least Q30
Consensus quality: 180287 bases at least Q20
Insert size: 165000; agarose-efp
Insert size: 182766; sum-of-colligs
Quality coverage: 5.9 in Q20 bases; sum-of-colligs
Quality coverage: 5.3 in Q20 bases; sum-of-colligs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

* be preserved.
1 6241: contig of 6241 bp in length
6342 6341: gap of 100 bp in length
6342 6341: gap of 100 bp in length
7729 7828: gap of 100 bp in length
7829 7828: gap of 100 bp in length
8848 8947: gap of 100 bp in length
8948 8947: gap of 100 bp in length
10137 10236: gap of 100 bp in length
10237 10236: gap of 100 bp in length
10237 10236: gap of 100 bp in length
11542 11641: gap of 100 bp in length
11642 11641: gap of 100 bp in length
13231 13330: gap of 100 bp in length
13331 13330: gap of 100 bp in length
14501 14600: gap of 100 bp in length
14601 14599: gap of 100 bp in length
15870 15969: gap of 100 bp in length
15970 15969: gap of 100 bp in length
17054 17153: gap of 100 bp in length
17154 17153: gap of 100 bp in length
18325 18424: gap of 100 bp in length
18425 18424: gap of 100 bp in length
19470 19569: gap of 100 bp in length
19570 19569: gap of 100 bp in length
21311 21410: gap of 100 bp in length
21411 21410: gap of 100 bp in length
22852 23051: gap of 100 bp in length
23052 23051: gap of 100 bp in length
25122 25221: gap of 100 bp in length
25222 25221: gap of 100 bp in length
27103 27202: gap of 100 bp in length
27203 27202: gap of 100 bp in length
30451 30550: gap of 100 bp in length
30551 30550: gap of 100 bp in length
129558 129558: gap of 99008 bp in length
129559 129558: gap of 99008 bp in length
147795 147795: contig of 1837 bp in length
147796 147895: gap of 100 bp in length
147896 147895: gap of 100 bp in length
175355 175355: contig of 27460 bp in length
175356 175355: gap of 100 bp in length
175456 175455: gap of 100 bp in length
184666: contig of 9211 bp in length.

FEATURES

source

1.184666 "Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-11516"
/clone.lib="RP11-11 Human Male BAC"

misc_feature

1.6241
/note="assembly-fragment"

clone.end:SP6
vector.start:left

misc_feature

6342.7728
/note="assembly-fragment"

misc_feature

7829.8847
/note="assembly-fragment"

misc_feature

8948.10136
/note="assembly-fragment"

misc_feature

10237.11541
/note="assembly-fragment"

misc_feature

11642.13230
/note="assembly-fragment"

misc_feature

13331.14500
/note="assembly-fragment"

misc_feature

14601.15869
/note="assembly-fragment"

misc_feature

15970.17053
/note="assembly-fragment"

misc_feature

17154.18324
/note="assembly-fragment"

misc_feature

18425.19469
/note="assembly-fragment"

misc_feature

19570.21310
/note="assembly-fragment"

misc_feature

21411.22951
/note="assembly-fragment"

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misc_feature      /note="assembly_fragment"
                  23052..25121
                  /note="assembly_fragment"
misc_feature      23222..27102
                  /note="assembly_fragment"
misc_feature      27203..30450
                  /note="assembly_fragment"
misc_feature      30551..129558
                  /note="assembly_fragment"
misc_feature      129659..147793
                  /note="assembly_fragment"
misc_feature      147896..175355
                  /note="assembly_fragment"
misc_feature      175456..184666
                  /note="assembly_fragment"
misc_feature      /note="assembly_fragment"
                  clone_end:t7
                  vector_side:right"
BASE COUNT      53667 a 37534 c 37634 g 53907 t 1904 others
ORIGIN
Query Match      1.2%: Score 25; DB 2; Length 184666;
Best Local Similarity 100.0%: Pred. No. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1860 AAAAAAATAAATAAAAAGAAAGA 1884
Db 109207 AAAAAAATAAATAAAAAGAAAGA 109231
|||||
AL392169 188120 bp DNA HTG 10-JUL-2001
DEFINITION      Homo sapiens chromosome 1 clone RP11-502F9, *** SEQUENCING IN
ACCESSION      AL392169
VERSION        AL392169.8 GI:13443436
KEYWORDS       HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE         human
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mclay/K.
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clone-requests@sanger.ac.uk
On Mar 24, 2001 this sequence version replaced gi:13398804.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA502F9
----- Summary Statistics
Assembly program: XGAP4; Version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 186026 bases at least Q40
Consensus quality: 186945 bases at least Q30
Insert size: 187620; sum-of-ctrls
Insert size: 190984; 3.5% error; agarose-fp
Quality coverage: 7.4ix in Q20 bases; sum-of-ctrls Quality
coverage: 7.54x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

```

```

* This record will be updated with the finished sequence
* as soon as it is available with the accession number will
* be preserved.
I 39912: contig of 39912 bp in length
* 39913 40012: gap of 100 bp
* 40013 70805: contig of 30793 bp in length
* 70806 70905: gap of 100 bp
* 70906 109829: contig of 38924 bp in length
* 109830 109829: gap of 100 bp
* 109930 151328: contig of 41399 bp in length
* 151329 151428: gap of 100 bp
* 151429 166455: contig of 15027 bp in length
* 166456 166555: gap of 100 bp
* 166556 188120: contig of 21565 bp in length.
location/Qualifiers
  1..188120
    organism="Homo sapiens"
    db_xref="taxon:9606"
    chromosome="1"
    clone_lib="RP11-502F9"
    clone_id="RP11-11.2"
    1..39912
    /note="assembly_fragment:02972
    fragment_chain:1"
    40013..70805
    /note="assembly_fragment:01087
    fragment_chain:1"
    70906..109829
    /note="assembly_fragment:01395
    fragment_chain:1"
    109930..151328
    /note="assembly_fragment:02833
    fragment_chain:2"
    151429..166455
    /note="assembly_fragment:00039
    fragment_chain:2"
    166556..188120
    /note="assembly_fragment:01325
    fragment_chain:2
    clone_end:SP6
    vector_side:right"
BASE COUNT      50383 a 39901 c 42215 g 55121 t 500 others
ORIGIN
Query Match      1.2%: Score 25; DB 2; Length 188120;
Best Local Similarity 100.0%: Pred. No. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1858 TAAAAAATAAATAAAAAGAAA 1882
Db 92166 TAAAAAATAAATAAAAAGAAA 92150
|||||
AC093278 193305 bp DNA HTG 16-AUG-2001
DEFINITION      Homo sapiens chromosome 5 clone RP11-389C8, WORKING DRAFT SEQUENCE.
ACCESSION      AC093278
VERSION        AC093278.1 GI:15193412
KEYWORDS       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
SOURCE         human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mclay/K.
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
Requests: clone-requests@sanger.ac.uk
On Mar 24, 2001 this sequence version replaced gi:13398804.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA502F9
----- Summary Statistics
Assembly program: XGAP4; Version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 186026 bases at least Q40
Consensus quality: 186945 bases at least Q30
Insert size: 187620; sum-of-ctrls
Insert size: 190984; 3.5% error; agarose-fp
Quality coverage: 7.4ix in Q20 bases; sum-of-ctrls Quality
coverage: 7.54x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

```

JOURNAL
Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 555797
Center clone name: RPCI-11_389C8

Summary Statistics
Consensus quality: 164321 bases at least Q40
Consensus quality: 179101 bases at least Q30
Consensus quality: 181596 bases at least Q20
Estimated insert size: 194450; agarose-IP estimation
Estimated insert size: 189505; sum-of-contigs estimation
Quality coverage: 2.96 in Q20 bases; agarose-IP estimation
Quality coverage: 3.04 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 39 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
1159: contig of 1159 bp in length
1160
1259: gap of unknown length
1260
1263: contig of 1004 bp in length
2264
2363: gap of unknown length
2364
3539: contig of 1176 bp in length
3540
3639: gap of unknown length
3640
5028: contig of 1389 bp in length
5029
5128: gap of unknown length
5129
6284: contig of 1136 bp in length
6285
6364: gap of unknown length
6365
7465: contig of 1101 bp in length
7466
7565: gap of unknown length
7566
9535: contig of 1970 bp in length
9536
9635: gap of unknown length
9636
11330: contig of 1635 bp in length
11331
11430: gap of unknown length
11431
13286: contig of 1856 bp in length
13287
13386: gap of unknown length
13387
15478: contig of 2092 bp in length
15479
15578: gap of unknown length
15579
18230: contig of 2652 bp in length
18231
18330: gap of unknown length
18331
20172: contig of 1842 bp in length
20173
20272: gap of unknown length
20273
22252: contig of 1980 bp in length
22253
22352: gap of unknown length
22353
24742: contig of 2390 bp in length
24743
24842: gap of unknown length
24843
28564: contig of 3722 bp in length
28565
28664: gap of unknown length
28665
32044: contig of 3380 bp in length
32045
32144: gap of unknown length
32145
35129: contig of 2985 bp in length
35130
35229: gap of unknown length
35230
37202: contig of 1973 bp in length
37203
37303: gap of unknown length
37304
41220: contig of 3918 bp in length
41221
41320: gap of unknown length
41321
45614: contig of 4294 bp in length
45615
45714: gap of unknown length
45715
50163: contig of 4449 bp in length
50164
50263: gap of unknown length
50264
54069: contig of 3806 bp in length
54169: gap of unknown length
54170
58033: contig of 4864 bp in length
59133: gap of unknown length
59034

59134 63714: contig of 4381 bp in length
63715 63814: gap of unknown length
63815 67443: contig of 3629 bp in length
67444 67543: gap of unknown length
67544 71100: contig of 3557 bp in length
71101 71200: gap of unknown length
71201 75142: contig of 3542 bp in length
75143 75242: gap of unknown length
75243 81250: contig of 6008 bp in length
81251 81350: gap of unknown length
81351 87500: contig of 6150 bp in length
87501 87600: gap of unknown length
87601 92831: contig of 5231 bp in length
92832 92931: gap of unknown length
92932 98789: contig of 3558 bp in length
98790 98889: gap of unknown length
98890 105146: contig of 6257 bp in length
105147 105246: gap of unknown length
105247 111043: contig of 5797 bp in length
111044 111143: gap of unknown length
111144 121308: contig of 10065 bp in length
121309 121308: gap of unknown length
121309 134109: contig of 12801 bp in length
134110 134209: gap of unknown length
134210 147170: contig of 12961 bp in length
147171 147270: gap of unknown length
147271 161279: contig of 14009 bp in length
161280 161379: gap of unknown length
161380 175379: gap of unknown length
175380 175479: contig of 14000 bp in length
193305: contig of 17826 bp in length.
Location/Qualifiers
1. 193305
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="RPI1-389C8"
/clone_lib="RPCI human BAC library 11"
/clone_lib="RPCI human BAC library 11"
/clone_lib="RPCI human BAC library 11"
/clone_lib="RPCI human BAC library 11"

BASE COUNT 54898 a 39605 c 39415 g 55580 t 3807 others
ORIGIN

Query Match 1.2%: Score 25; DB 2; Length 193305;
Best Local Similarity 100.0%; Pred. NO. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1860 AAAAAAAAAATTAAGAAAAAGA 1884
Db 177762 AAAAAAAAAATTAAGAAAAAGA 177786

RESULT 9
AL353741
LOCUS
DEFINITION
ACCESSION
AL353741
VERSION
AL353741.16 GI:12584694
KEYWORDS
HTG.
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 199517)

AUTHORS
TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jan 28, 2001 this sequence version replaced gi:12580980.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the

variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at <http://www.sanger.ac.uk/Projects/Celegans/wormpep> This sequence was generated from part of bacteriophage clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr9> Rpl1-575C20 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

FEATURES

SOURCE

1. 199517

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="9"

/clone="RPI1-575C20"

/clone_1lb="RPCI-11.2"

/clone_1lb="RPCI-11.2"

/note="Single clone region. Assembly confirmed by restriction digest data."

/note="Single clone region. Assembly confirmed by restriction digest data."

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/note="Single clone region. Assembly confirmed by restriction digest data."

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/note="Single clone region. Assembly confirmed by restriction digest data."

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/note="Single clone region. Assembly confirmed by restriction digest data."

/note="Single clone region. Assembly confirmed by restriction digest data."

/note="Single clone region. Assembly confirmed by restriction digest data."

/note="Single clone region. Assembly confirmed by restriction digest data."

Contact: humquerry@sanger.ac.uk
Project Information
Center Project name: BA380822
Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 21006; bases at least Q40
Consensus quality: 210412; bases at least Q30
Consensus quality: 210565; bases at least Q20
Insert size: 210871; sum-of-contigs
Insert size: 208059; 5.5% error; agarose-ff
Quality coverage: 8.15x in Q20 bases; sum-of-contigs Quality
coverage: 8.25x in Q20 bases; agarose-ff

NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

FEATURES

SOURCE

1. 211271

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

/clone="RPI1-380B22"

/clone_1lb="RPCI-11.2"

/clone_1lb="RPCI-11.2"

/note="assembly-fragment:02974"

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Query Match
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1858 TAAAAAATTAATTAAGAGAAA 1882
|||||
Db 67484 TAAAAAATTAATTAAGAGAAA 67460

FEATURES

SOURCE

1. 9007

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

/clone="RPI1-380B22"

/clone_1lb="RPCI-11.2"

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/note="assembly-fragment:02974"

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/note="assembly-fragment:02974"

Query Match
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1858 TAAAAAATTAATTAAGAGAAA 1882
|||||
Db 67484 TAAAAAATTAATTAAGAGAAA 67460

FEATURES

SOURCE

1. 9007

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

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/clone_1lb="RPCI-11.2"

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Query Match
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1858 TAAAAAATTAATTAAGAGAAA 1882
|||||
Db 67484 TAAAAAATTAATTAAGAGAAA 67460

FEATURES

SOURCE

1. 9007

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="1"

/clone="RPI1-380B22"

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DEFINITION P. falciparum GBP2 gene.
ACCESSION X69769
VERSION X69769.1 GI:9892
KEYWORDS GBP2 gene.
SOURCE malaria parasite P. falciparum.
ORGANISM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 1366)
AUTHORS Knapp, B.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-1992) B. Knapp, Behringwerke AG, Research Laboratories, P.O. Box 11 40, D-3550 Marburg/Lahn, FRG
REFERENCE 2 (bases 1 to 1366)
AUTHORS Rudolph, B., Nolte, D. and Knapp, B.
TITLE Isolation of a third member of the plasmodium falciparum glycoprotein-binding protein gene family
JOURNAL Mol. Biochem. Parasitol. 68 (1), 173-176 (1994)
MEDLINE 95198770
FEATURES
source
1. .1366
/organism="Plasmodium falciparum"
/strain="FCBR (Columbia)"
/db_xref="taxon:5833"
/dev_stage="blood"
134. .322
/gene="GBP2"
/number=1
/product="GBP2"
134. .1309
/gene="GBP2"
join(224. .322, 479. .1309)
/gene="GBP2"
/product="GBP2"
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/protein_id="CAA49424.1"
/db_xref="GI:9893"
/db_xref="SPRMBL:Q25859"
/translation="MDVQERNKRSLSFHSKQIILFGIITYVALLVNYICGKXQO
DADYSETEGVLAQCEFACTNNTKTSLRCAQTTSADPEQIMKAAADPEYRKHI
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323. .478
/gene="GBP2"
/number=1
479. .1309
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/number=2
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BASE COUNT 551 a 219 c 201 g 395 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1859 AAAAAAAAAATAAATAAGAAAA 1882
DB 2 AAAAAAAAAATAAATAAGAAAA 25

RESULT 12
LOCUS PFCBP21 1366 bp DNA INV 15-DEC-1994
DEFINITION P. falciparum FCBR (Columbia) GBP2 gene exons 1 and 2.
ACCESSION X79836
VERSION X79836.1 GI:509184
KEYWORDS GBP2 gene.
SOURCE malaria parasite P. falciparum.
ORGANISM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE 1 (bases 1 to 1366)
AUTHORS Rudolph, B., Nolte, D. and Knapp, B.
TITLE Isolation of a third member of the Plasmodium falciparum glycoprotein-binding protein gene family
JOURNAL Mol. Biochem. Parasitol. 68 (1), 173-176 (1994)
MEDLINE 95198770
REFERENCE 2 (bases 1 to 1366)
AUTHORS Knapp, B.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-1994) B. Knapp, Behringwerke AG, Research Laboratories, P.O. Box 11 40, 3550 Marburg/Lahn, FRG
FEATURES
source
1. .1366
/organism="Plasmodium falciparum"
/strain="FCBR (Columbia)"
/db_xref="taxon:5833"
/dev_stage="blood stage"
join(134. .322, 479. .1306)
/gene="GBP2"
join(134. .322, 479. .1306)
/gene="GBP2"
134. .322
/gene="GBP2"
/number=1
323. .478
/number=1
479. .1306
/gene="GBP2"
/number=2
BASE COUNT 551 a 219 c 201 g 395 t
ORIGIN

Query Match 1.1%; Score 24; DB 3; Length 1366;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1859 AAAAAAAAAATAAATAAGAAAA 1882
DB 2 AAAAAAAAAATAAATAAGAAAA 25

RESULT 13
LOCUS AC019982/c 8077 bp DNA HTG 03-JAN-2000
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
ACCESSION AC019982
VERSION AC019982.1 GI:6664915
HTG: HTGS_PHASE2.
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 8077)
AUTHORS Adams, M. and Venter, J.C.
TITLE Direct Submission
JOURNAL Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
COMMENT This sequence was identified as CDM:10211617 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source
1. .8077
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
BASE COUNT 2477 a 1794 c 1761 g 2045 t
ORIGIN

SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 114898)
AUTHORS Martindale,D.W., Wilson,M.D., Wang,D., Burke,R.D., Chen,X.,
Duronio,V. and Koop,B.F.
TITLE Comparative genome sequence analysis of the Williams syndrome
region (LIMK1-RFC2) of human chromosome 7q11.23
JOURNAL Mamm. Genome 11 (10), 890-898 (2000)
MEDLINE 20458868
PUBMED 11003705
REFERENCE 2 (bases 1 to 114898)
AUTHORS Martindale,D.W., Wilson,M.D. and Koop,B.F.
TITLE Direct Submission
JOURNAL Submitted (01-APR-1999) Department of Biology, Centre for
Environmental Health, University of Victoria, P.O. Box 3020,
Victoria, BC V8W 3N5, Canada
FEATURES
source
1. 114898
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/organism="Mus musculus"
/strain="ES-129/SV01"
/db_xref="taxon:10090"
/clone="Genome Systems Inc BAC17511"
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20947..21153,22176..22281,22391..22557,25458..25641,
26178..26264,27155..27286,29309..29368,29613..29678,
31468..31624,33507..33562,33821..33978,34086..35418)
/gene="Limk1"
/product="Lim-kinase1"
2873..35418
/gene="Limk1"
join(3076..3130,4731..4827,18321..18459,18691..18800,
20947..21153,22176..22281,22391..22557,25458..25641,
26178..26264,27155..27286,29309..29368,29613..29678,
31468..31624,33507..33562,33821..33978,34086..35428)
/gene="Limk1"
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/product="Lim-Kinase1"
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KHPEPTCLACGNFTGDDDTIVLHSHKLYCCGYVTVTPVTELLPSPSHIP
HTVTLVSPASAGKRLSVSIDPFGPGCTESHSTVRVQGDPCGMSDVNSIH
VGRRIEINGTPIRNPVLEIDLIIQETSRLQTLLEHDPHDSLGHSEVSPSSLP
VHTPSQASASARQKPYRLSCSIDTSPGTSLSAPASQKDLGRSESLAVVCRHRL
RPSDLHGEVLGKGCPCQAIVYHRETGEVWMLKILRFDETRTFLEKVVACLE
HPVNLFTGVLVYDKRLNFTTEVYIGGTLRGILIKMDSQYPMSPQVPAKDIASGMA
LHSMNTHHNDHNSHCLVRENRYVADGLRIKMWIDENQSEDLRSIKKDRKRYT
VGNPTMAPEMNGRSYDEKDVSEFGVLCIEITIGRNADPDYLPRTMDGLVNRG
LDRICPNCPSPEFTVRCDDLPKRSFVLEIQLLEITLMLHLSGHLPLGPLEOL
ERGEWETRRGESSLPAPHEVPD"
/gene="Limk1"
35395..35400
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66975..67034,69389..69526,69827..71599)
/gene="Wbscr1"
/product="Wbscr1"
join(52154..52241,63700..63887,65870..65934,66013..66109,
69389..69526,69827..71599)
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/product="Wbscr1 alternative spliced product"
52154..71599
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69389..69526,69827..69966)
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/product="Wbscr1 alternative spliced product"
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/translation="MADFDTYDRAISSFGGGRSGSAGHSRQKRLPEPYTA

CDS
YVGNLFNTVGGIDDAIFKDLISRSVRLVBDKIDKFKGCFYEPDEVDLKEALTYD
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GSRKDPPLPGSMMDRPEEERARPRQLKPRVATPLNQVNPNSAIFGARGP
REEVQKQKE
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66975..67034,69389..69526,69827..69966)
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/product="Wbscr1"
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/db_xref="GI:4972950"
/translation="MADFDTYDRAISSFGGGRSGSAGHSRQKRLPEPYTA
YVGNLFNTVGGIDDAIFKDLISRSVRLVBDKIDKFKGCFYEPDEVDLKEALTYD
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GSRKDPPLPGSMMDRPEEERARPRQLKPRVATPLNQVNPNSAIFGARGP
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71576..71581
/gene="Wbscr1"
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86674..86729,87995..88054,88305..88376,88806..88914,
90506..91457)
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85083..85114,85513..85543,86674..86729,87995..88054,
88305..88376,88806..88888)
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/db_xref="GI:8470891"
/translation="MSAELELMPYSGLLLLLTATATLVCYHGRPGVKNREKYEOR
NQENQSSAAQOTYSLARQVPGQMTAPKSPERKNKLFHLLGSDNPDAAY
DIPFNLYMGGEQKPSDEDDNSYENLVKPSFTPEGVDVCDYONVSIHQWRS
KRTGAPMLSGSPDEPDYVNGDVAALNT"
join(82571..82667,83281..83320,84654..84697,84915,
85083..85114,85394..85429,85513..85543,86674..86729,
87995..88054,88305..88376,88806..88888)
/gene="Wbscr5"
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DIPFNLYMGGEQKPSDEDDNSYENLVKPSFTPEGVDVCDYONVSIHQWRS
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ONSVSQHPDAIVDPIPTNRYVNGCRKSPEDDPSYVNGDVAALNT"
KNSVSHQWRESKRTWGAPWSLSSGSPDEPDYVNGDVAALNT"
complement(join(93152..93630,94484..94597,96116..96196,
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102020..102126,102508..102549,104514..104583,
108595..108710))
/gene="Rfc2"
/product="replication factor C, 40kDa subunit"
complement(93152..108710)
/gene="Rfc2"
/gene="Rfc2"
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complement(join(93520..93630,94484..94597,96116..96196,
97205..97270,98133..98290,100260..100360,100502..100603,
102020..102126,102508..102549,104514..104583,
108595..108692))
/gene="Rfc2"
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/product="replication factor C, 40kDa subunit"
/protein_id="AAD34861.1"

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/db.xref="GI:4972952"  
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IVGNEDTVSRLEVFARREGNVPNIIITAGPCTGKTSTICLARALIGPALKDAVEINA  
SNRGIDVVRNKKIKMEAQKVTLLPKGRHRTIILDEADSTIDGAQALRTMETISKTT  
RFLACNASDKLIEPIQSRCAVLRTKLTDQAVLRMLNVIKEKVPYTDGLEALIF  
TAQGMROALNNLOSTFSGFGYINSENVKVCDEPHPLLVEMIQHCVDANIDEAYKI  
LAHLMHIGYSPEDVIGNIFRYCKTFPMAEYLKLEFIKEIGYTHMKVAGVNSLLQMG  
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BASE COUNT      28567 a 28771 c 28573 g 28987 t  
ORIGIN
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Query Match      1.1%; Score 24; DB 10; Length 114898;  
Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1861 AAAAAATTAATAAAGAAAAAGA 1884  
Db 33257 AAAAAATTAATAAAGAAAAAGA 33280
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Search completed: April 16, 2002, 18:18:06
Job time: 6547 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 16, 2002, 16:46:45 ; Search time 120.58 Seconds

(without alignments)
14859.925 Million cell updates/sec

Title: US-09-636-826-1

Sequence: 1 GATATCACACATTTCGTCAT.....TCGGCTTCTGGGCTGCTCT 2090

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 930621 seqs, 428662619 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

N.Geneseq_1101.*
1: /SIDS2/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseqn/NA1982.DAT.*
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* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2090	100.0	2090	22	AA61197
2	23	1.1	162450	21	AA286967
3	22	1.1	543	22	AAH12273
4	22	1.1	1562	22	AAF32540
5	22	1.1	3021	22	AAF32539
6	22	1.1	6542	22	AAF32538
7	22	1.1	50000	21	AA64140
8	21	1.0	183	22	AA161659
9	21	1.0	885	22	AAH04005
10	21	1.0	1381	15	AAQ77883
11	21	1.0	1381	17	AA27765

c 12	21	1.0	1418	17	AA27738	Neural thread prot
c 13	21	1.0	1423	21	AA297059	Human secreted pro
c 14	21	1.0	1692	21	AA18279	Lung cancer associ
c 15	21	1.0	1737	21	AA256739	Human transmembran
c 16	21	1.0	513445	22	AA161373	Soybean 318013 reg
c 17	20	1.0	182	22	AA161749	Soybean 515002 reg
c 18	20	1.0	197	21	AA05247	Human secreted pro
c 19	20	1.0	296	21	AA400620	Human colon cancer
c 20	20	1.0	319	22	AAH88025	Peppermint plant o
c 21	20	1.0	332	21	AA19809	Human secreted pro
c 22	20	1.0	404	18	AA19381	Murine metastatic
c 23	20	1.0	445	21	AA15573	Human prostate can
c 24	20	1.0	474	22	AA138578	Probe #7264 used t
c 25	20	1.0	568	21	AA188015	568 bp Candida alb
c 26	20	1.0	598	21	AA457965	598 bp Candida alb
c 27	20	1.0	633	13	AA020241	Pis16 gene. Plasm
c 28	20	1.0	781	20	AA215116	Human gene express
c 29	20	1.0	946	21	AA58016	946 bp Candida alb
c 30	20	1.0	2733	19	AAV13832	Homo sapiens telom
c 31	20	1.0	2733	19	AAV05369	Human telomerase p
c 32	20	1.0	2809	22	AAH14068	Human cDNA sequenc
c 33	20	1.0	4233	21	AA290158	Rat mdrlb2 (multis
c 34	20	1.0	4233	22	AA274958	Rat mdrlb2 multidr
c 35	20	1.0	9789	17	AA11852	cDNA encoding plas
c 36	20	1.0	127197	22	AA161370	Soybean 515002 reg
c 37	19	0.9	47	21	AA268270	Human map-related
c 38	19	0.9	62	21	AA44614	Au rich sequence i
c 39	19	0.9	212	21	AA14970	Human secreted pro
c 40	19	0.9	245	21	AA14835	Human secreted pro
c 41	19	0.9	292	21	AA11355	Aspergillus niger
c 42	19	0.9	312	22	AAH11673	Human cDNA clone (
c 43	19	0.9	313	21	AA43641	Human secreted exp
c 44	19	0.9	363	21	AA13310	Human secreted pro
c 45	19	0.9	403	22	AAH29465	Drosophila melanog

ALIGNMENTS

RESULT 1	
ID	AA61197 standard; DNA; 2090 BP.
XX	
AC	AA61197;
XX	
DT	23-MAY-2001 (first entry)
XX	
DE	B. vulgaris V-ATPase subunit C isoform 2 promoter DNA.
XX	
KW	Promoter; V-ATPase; subunit C; isoform 2; plant; transgenic plant;
KW	V-type adenosine triphosphatase; stress resistance; insect resistance;
KW	herbicide resistance; disease resistance; salt stress; constitutive;
KW	nutrient deficiency; injury; infection; selection marker; ss.
XX	
OS	Beta vulgaris.
XX	
PN	W0200114572-A2.
XX	
PD	01-MAR-2001.
XX	
PF	10-AUG-2000; 2000MO-EP07774.
XX	
PR	26-AUG-1999; 99DE-1040648.
XX	
PR	26-AUG-1999; 9905-0150887.
XX	
PA	(BADI) BASF AG.
XX	
PI	Duvenig E, Rausch T;
XX	
DK	WPI; 2001-218455/22.
XX	
PT	New DNA construct containing a plant V-type adenosine triphosphatase
PT	promoter, useful for recombinant protein expression or producing

PT stress-resistant plants -
XX
PS Claim 6; Page 65-66; 69pp; German.
XX

CC This invention describes a novel DNA construct (I) which comprises a
CC plant V-ATPase (V-type adenosine triphosphatase) promoter (P), or its
CC functional equivalent, coupled to a heterologous gene. The invention also
CC describes (1) a polynucleotide (II) containing the sequence of (P) from
CC the Beta vulgaris V-ATPase subunit c isoform 2 (2090 bp sequence (1)),
CC reproduced), or its functional equivalents; (2) a recombinant vector
CC containing (I); (3) a microorganism transformed with the vector of (2);
CC (4) a transgenic plant cell or protoplast that contains (I); (5) a
CC transgenic plant containing (I) in its genome; (6) controlling (M1)
CC expression of (II) in a plant cell or protoplast by transforming with (I)
CC then exposing to an (a)biotic stress that controls expression of (II);
CC (7) method (M2) similar to (M1), but applied to regenerated transgenic
CC plants; (8) preparation (M3) of recombinant proteins (IV) by methods (M1)
CC and (M2); (9) (II) produced by method (M3); and (10) plant cells or
CC protoplasts, and regenerated plants, transformed with (I) and resistant
CC to (a)biotic stresses. (I), and (II) are used to direct expression of
CC recombinant proteins in plants, or their cells or protoplasts. (III) is
CC used to provide expression of genes in plants under (a)biotic stresses,
CC such as genes that impart resistance to insects, herbicides, diseases, or
CC selection genes. (IV) is used to produce plants with increased resistance
CC to stress (especially salt but also nutrient deficiency, injury,
CC infection, presence of herbicides). P are very strong, constitutive
CC promoters, effective in all parts of a plant, and they become more
CC active, or are not repressed, under conditions of stress, so are better
CC than known plant or viral promoters for expressing selection markers and
CC resistance genes.
CC
XX

Sequence 2090 BP; 794 A; 354 C; 271 G; 671 T; 0 other;

Query Match 100.0%; Score 2090; DB 22; Length 2090;
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;
Matches 2090; Conservative 0; Indels 0;

QY 1 GATATCACACATTCGTCATCGAGCATTTGGCACTTCAATAGGTACGTAACTCTTT 60
DB 1 gatacacacatctgcacatcgacgattgsgaacttcaaatagtagtaattcttt 60
QY 61 AATCTTCAAGTTATTTACATTTAGTACTATTATGTATGAAAAAGGAGTAATA 120
DB 61 aatcttcaagttatctacatgtagcagactatgtagtgaataaagagataaata 120
QY 121 GSAATTAGTAAAAAGGCTTTATATATATAGACTTAATTTGATTCATTTATAT 180
DB 121 gsaattagtgaaaaagggtgttatataaatagacttaattgattcatcttcataat 180
QY 181 CTGAAAACAGGTATGTAATTTGATTCATTTATGACATGATGAAAAATTACGA 240
DB 181 ctgaaaacaaagtgatgtaaatltgattcatatgacacgtatgaaaaattaca 240
QY 241 TTATCTCTTTTATTAATTCATATTAATTTTGGCCAAACTTTGCAAAATATC 300
DB 241 ttatctcttttttataatccataataaatlttgcocaaactttgcaaaatatac 300
QY 301 CATGTTCGGAATTAATTTTGAATAACAAATATCAAACTTTTGGCAACAATT 360
DB 301 catgttcggaattaaatttgaataacaaataatcaaaacttttgcgaaacttt 360
QY 361 TACAAATATCCATTTTGAATAAAAAATTTACATTAAGTGGCAATCAATTTGTAT 420
DB 361 tacaaatatacttttcgaaaaataatttaacttaacttgcgaaatcaaatgtat 420
QY 421 GAAAAATTTAAATTTCTTTACCTATTAATGAACCTCAAGTGTTAAATTTAGAAA 480
DB 421 gaaaaatttaaatcttcttcacctataatgaaactcaagtgtaaaatlttagaaa 480
QY 481 GGAGAAAAATTAATAATGACATTTGATGCAAAATCAATTTGTATGAAAAACTTAAA 540
DB 481 ggagaaaaataataatgacatcttcatcgaaatcaaatgtgtatgaaaaacttaaa 540

QY 541 TTTATTTTAAATATTAATGAAATTCAAAGCTTTAAATTTAGAAAAAGAGAAAAATTA 600
DB 541 tttattttaataataatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 600
QY 601 AATGACCATTTCTTCAATTAATTCGATTTGTATGAAAAATTTAAATTTTATTTCAATA 660
DB 601 aatgaccatttcaataataatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 660
QY 661 TAAATGAACTCAAGTGTACATTTAGAAAAAGGAAAAATTTAAATGATGAAAAATT 720
DB 661 taatgaaactcaagtgtaacatttagaaaggaataatgaaatgaaatgaaatgaaat 720
QY 721 GTAAATATCAATTTTGAATCAGAAATTTAGAGTTATACAGAGAAAAAAACGAAAT 780
DB 721 gtaaaatacaatttggaatacaaatlttagaaatgaaatgaaatgaaatgaaatgaaat 780
QY 781 GTCTTATCTTTTGGTACAAATTTTGGGATCATTAAGAAATTTACTGAAATGCATATCA 840
DB 781 gtcttatacttttgggtacaaatttgggataataaagaataatgaaatgaaatgaaat 840
QY 841 AACTATTTATTAATTAATAAATGATTAACCAAAAAAGAAAGAAACATGAGATATTC 900
DB 841 aactatataataatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaatgaaat 900
QY 901 GTAAAGAACATCAATCTGATTAATAAAGAACATGCCATTTAGATTTGAGAAACAAAA 960
DB 901 gtaagaacatcatatcatgattataaagaacatgcatatgaaatgaaatgaaatgaaat 960
QY 961 ACTTTTCAAAATCCAAAAATGATTAACCAATCAACAAAGAAATGAAATCTTATCA 1020
DB 961 actttaaaaaatcaaaaaatgatacaacaataaagaataaagaataaatacttaacca 1020
QY 1021 CAAATGAGGTGACTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
DB 1021 caaatgaggtgacttaataataataataataataataataataataataataataata 1080
QY 1081 AGSCCTAAAAATATCATCGACGATTCGCTGCACAAAAAGCTAGTGTATATACAA 1140
DB 1081 agscctaaaaatatacatcgacgattcgctgcacaaaagactagtgtaataatacaaa 1140
QY 1141 GTCAACAACTCAGACAGTATTTCAATTTAGGTCATTTGATTTGATTTGATTTGATTT 1200
DB 1141 gtcaacaaactcagacagatttcaattttaggtccatcttggatggcgtaaaacttttc 1200
QY 1201 CCGAACAATATTTTCTCATTTTATTTAGTTTATTTATTTATTTATTTATTTATTTAT 1260
DB 1201 ccgaacaataattttctcattttttagttttcatgtttgtttgaaataaagatgttaa 1260
QY 1261 AACGTTTTCCTGGGGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
DB 1261 aacgttttccctggggtaaatataataataataataataataataataataataataata 1320
QY 1321 AATGAAGGAAATGTTTCTTATCTGTTTATTTATTTATTTATTTATTTATTTATTTAT 1380
DB 1321 aatgaaggaaatgtttcttattctgttttatacttcccttccatcttccatcttcc 1380
QY 1381 TTCCCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1440
DB 1381 ttcccttttattttattttattttattttattttattttattttattttattttatttt 1440
QY 1441 ACTAATTTGGAATTTGTTTCCATTTGTAATTTGTTTCCATGAAATTCATTTTACT 1500
DB 1441 actaattttgaaatttggtttccatttgtaatttggtttccatgaaatctattttact 1500
QY 1501 GAAATGTTTATACCTTACCAACAGAGCTTCGTTGCAATGATGATGATGATGATGATG 1560
DB 1501 gaaatgtttataccttaccacacagagcttcggttgcaatgattgattgattgattgatt 1560
QY 1561 CAAATTCGAAATGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1620
DB 1561 caaattcgaaatggttttattttattttattttattttattttattttattttatttt 1620

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QY 1621 AACTATGTCGTACCCCTAAAGATGATATGTAATTAACCTTGAGGCGCTTGGCTAA 1680
    |||||||
Db 1621 aactatgctgtacccctaaagatgatatgttaaaccttgaggcttgcttaaa 1680
QY 1681 AAAAGTCCACGACGCCCCCATTTGTAGCTCCCAAAACGACGAAATTTCTGGTACTATT 1740
    |||||||
Db 1681 aaaagtccacgacgcccccatctaggtcccaaacacgaattcttgtaactatt 1740
QY 1741 CCAAAACAAATAAACACACTCTGTATCAACGACGAAAAATAAATATTTTGTGTTT 1800
    |||||||
Db 1741 ccaaaaataaataaacactctgtatcaacgaagaaaaataaacatatttggltt 1800
QY 1801 CTCGCCAATTTTTCATTTTAATTTATGACGGGAAAGTACCAATTAATTCATGACGGTAA 1860
    |||||||
Db 1801 ctcccaattttcatltaattatatacgggaagatcaataatcatcaaggttaa 1860
QY 1861 AAAAATAAATAAATAAAGATAAGTATTAACAAAAGAAATTTGTTCTTCTACATAC 1920
    |||||||
Db 1861 aaaaaataaataaataaagataagataataaacaagaattgtcttcttccatc 1920
QY 1921 CTCATATTTTCATCCACGCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1980
    |||||||
Db 1921 ctcatattcatccacgctctcttctctctctctctctctctctctctctctccaga 1980
QY 1981 TCGGATCAAGCAATTTGATCGACACCTTCGATCATACCAATCAAAAAAATGTCAGAG 2040
    |||||||
Db 1981 tcggatcaagcaatctcgcacacccctccgataccacccaacaaatcgtcaacag 2040
QY 2041 TCTTTAAAGGCGATGAAGAACGCGCGCTTCTTGGCTTGTGGTGTGCT 2090
    |||||||
Db 2041 tctttaagcgatgaagaaagcgcgcttcttggtgtgtgtgt 2090

RESULT 2
AAZ86967
ID AAZ86967 standard; DNA: 162450 BP.
XX
AC AAZ86967;
XX
DT 16-MAY-2000 (first entry)
XX
DE Retinoblastoma binding protein-7 genomic DNA sequence.
XX
KW RBP-7; retinoblastoma binding protein-7; abnormal cell proliferation;
KM diagnosis; therapy; cell differentiation; thyroid hyperplasia; psoriasis;
KW benign prostate hypertrophy; cancer; sarcoma; neoplasm; leukaemia;
KW lymphoma; ds.
XX
OS Homo sapiens.
XX
PN M020000607-A1.
XX
PD 06-JAN-2000.
XX
PE 30-JUN-1999; 99MO-IB01242.
XX
PR 30-JUN-1998; 9805-0091315.
XX
PR 10-DEC-1998; 9805-0111909.
XX
PA (GEST ) GENSET.
XX
PI Bouguetieret L;
XX
DR WPI: 2000-117170/10.
XX
PT Novel nucleic acid and polymorphic markers used for diagnosis of
PT diseases, especially those involving abnormal cell proliferation and
PT differentiation -
XX
PS Claim 1; Page 118-163; 223pp. English.
XX
CC This sequence represents the retinoblastoma binding protein-7 (RBP-7)
CC genomic sequence of the invention. The RBP-7 coding sequence and

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CC regulatory sequences are useful for the recombinant production of the
CC protein and for expressing heterologous nucleic acids. Primers and
CC probes derived from the RBP-7 nucleotide sequence (e.g. AAZ87035-287099)
CC are useful for DNA amplification and detection methods. RBP-7 diallelic
CC markers (see AAZ86993-287034) are useful for diagnosis of disease
CC related to alteration in the regulation or in the coding regions of the
CC RBP-7 gene and for prognosis/diagnosis of an eventual treatment with
CC therapeutic agents, especially agents acting on pathologies involving
CC abnormal cell proliferation and/or differentiation, these include
CC thyroid hyperplasia, psoriasis, benign prostate hypertrophy, cancers,
CC including breast cancer, sarcomas and other neoplasms, bladder cancer,
CC colon cancer, lung cancer, prostate cancer, various leukaemias, and
CC lymphomas. RBP-7 antibodies are useful as diagnostic agents.
XX
SQ Sequence 162450 BP; 45465 A; 30661 C; 32637 G; 53673 T; 14 other;

Query Match 1.1%; Score 23; DB 21; Length 162450;
Best Local Similarity 100.0%; Pred. No. 0.99;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1858 TAAAAAATAAATAAATAAAGAA 1880
    |||||||
Db 137096 taaaaataaataaataaagaa 137118

RESULT 3
AAH12273
ID AAH12273 standard; cDNA; 543 BP.
XX
AC AAH12273;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA clone (3'-primer) SEQ ID NO:9108.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PE 28-JUL-2000; 2000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
XX
PR 27-AUG-1999; 99JP-0300253.
XX
PR 11-JAN-2000; 2000JP-0118776.
XX
PR 02-MAY-2000; 2000JP-0183767.
XX
PR 09-JUN-2000; 2000JP-0241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI: 2001-318749/34.
XX
PE Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
PS Claim 3; SEQ ID 9108; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the

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CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AA92446 to
 CC AA95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.

XX Sequence 543 BP; 176 A; 115 C; 70 G; 176 T; 6 other;

Query Match 1.1%; Score 22; DB 22; Length 543;

Best Local Similarity 100.0%; Pred. No. 3.4; Mismatches 0; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 420 TGAATAATTAATAATTCCTT 441
 DB 511 tgaataatataatttcctt 532

RESULT 4

AA932540/C
 ID AAF32540 standard; DNA; 1562 BP.

XX AAF32540;

DT 19-APR-2001 (first entry)

DE Mouse P/Q-type calcium channel upstream sequence SEQ ID NO:3.

XX Mouse; P/Q-type calcium channel upstream sequence; brain; neuron;

KW P/Q-type calcium channel $\alpha 1A$; cerebral neuron; ds.

XX Mus sp.

PN JP2000316583-A.

PD 21-NOV-2000.

PF 14-MAY-1999; 99JP-0133421.

PR 14-MAY-1999; 99JP-0133421.

PA (EISA) EISAI CO LTD.

DR WPI; 2001-066178/08.

XX A vector expressing specifically in brain

PS Claim 3; Page 12; 23pp; Japanese.

CC The present sequence represents a mouse P/Q-type calcium (Ca) channel
 CC upstream sequence. The present invention describes a method which can
 CC be used for expressing a heterologous gene in neurons especially
 CC cerebral neurons.

XX Sequence 1562 BP; 274 A; 482 C; 412 G; 394 T; 0 other;

Query Match 1.1%; Score 22; DB 22; Length 1562;

Best Local Similarity 100.0%; Pred. No. 3.3; Mismatches 0; Indels 0; Gaps 0;

QY 1863 AAAATAAATAAAGAAAGA 1884
 |||

DB 1213 AAAATAAATAAAGAAAGA 1192

RESULT 5

AA932539/C
 ID AAF32539 standard; DNA; 3021 BP.

XX AAF32539;

DT 19-APR-2001 (first entry)

DE Mouse P/Q-type calcium channel upstream sequence SEQ ID NO:2.

XX Mouse; P/Q-type calcium channel upstream sequence; brain; neuron;

KW P/Q-type calcium channel $\alpha 1A$; cerebral neuron; ds.

XX Mus sp.

PN JP2000316583-A.

PD 21-NOV-2000.

PF 14-MAY-1999; 99JP-0133421.

PR 14-MAY-1999; 99JP-0133421.

PA (EISA) EISAI CO LTD.

DR WPI; 2001-066178/08.

XX A vector expressing specifically in brain

PS Claim 2; Page 10-11; 23pp; Japanese.

CC The present sequence represents a mouse P/Q-type calcium (Ca) channel
 CC upstream sequence. The present invention describes a method which can
 CC be used for expressing a heterologous gene in neurons especially
 CC cerebral neurons.

XX Sequence 3021 BP; 693 A; 810 C; 707 G; 811 T; 0 other;

Query Match 1.1%; Score 22; DB 22; Length 3021;

Best Local Similarity 100.0%; Pred. No. 3.2; Mismatches 0; Indels 0; Gaps 0;

QY 1863 AAAATAAATAAAGAAAGA 1884
 DB 2672 AAAATAAATAAAGAAAGA 2651

RESULT 6

AA932538/C
 ID AAF32538 standard; DNA; 6542 BP.

XX AAF32538;

DT 19-APR-2001 (first entry)

DE Mouse P/Q-type calcium channel upstream sequence SEQ ID NO:1.

XX Mouse; P/Q-type calcium channel upstream sequence; brain; neuron;

KW P/Q-type calcium channel $\alpha 1A$; cerebral neuron; ds.

XX Mus sp.

PN JP2000316583-A.

PD 21-NOV-2000.

PF 14-MAY-1999; 99JP-0133421.

PR 14-MAY-1999; 99JP-0133421.

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XX      (EISA ) EISA1 CO LTD.
PA      WPI: 2001-066178/08.
DR      A vector expressing specifically in brain
XX      -
XX      Claim 1; Page 8-10; 23pp; Japanese.
PS
XX      The present sequence represents a mouse P/Q-type calcium (Ca) channel
CC      upstream sequence. The present invention describes a method which can
CC      be used for expressing a heterologous gene in neurons especially
CC      cerebral neurons.
XX
SQ      Sequence 6542 BP; 1642 A; 1688 C; 1567 G; 1645 T; 0 other;

Query Match          1.1%; Score 22; DB 22; Length 6542;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1863 AAAATAAATAAATAAAGAAAAGA 1884
        |||||||||||||||||||
DB      5925 AAAATAAATAAATAAAGAAAAGA 5904

RESULT 7
AAA64140
ID      AAA64140 standard; DNA; 50000 BP.
XX
AC      AAA64140;
XX
DT      20-DEC-2000 (first entry)
XX
DE      Nucleotide sequence of a beta-tubulin antigen.
XX
KM      Beta-tubulin antigen; inner ear protein; Meniere's disease; autoantibody;
KM      chronic ear disease; autoimmune disease; ss.
XX
OS      Homo sapiens.
XX
PN      WO200050593-A1.
XX
PD      31-AUG-2000.
XX
PF      25-FEB-2000; 2000MO-US04795.
XX
PR      25-FEB-1999; 99US-0121549.
XX
PA      (UYTE-) UNIV TENNESSEE RES CORP.
XX
PI      Yoo TJ;
XX
DR      WPI: 2000-558400/51.
XX
XX      New beta-tubulin antigen in the membranous structure of the inner ear,
PT      reactive with antibodies of patients with Meniere's disease, for
PT      diagnosing Meniere's disease and distinguishing this disease from other
PT      autoimmune ear diseases
XX
PS      Claim 3; Page 74-97; 115pp; English.
XX
CC      The present sequence encodes a beta-tubulin antigen. The protein is
CC      an antigen of the membranous structure of the inner ear protein, and
CC      is reactive with antibodies from patients having Meniere's disease.
CC      Meniere's disease is a chronic ear disease with unknown etiology.
CC      Serum from patients suffering from this disease contain autoantibodies
CC      against a 30 kDa cochlear protein antigen. The disease is believed to be
CC      an autoimmune disease. The beta-tubulin antigen is useful as a target
CC      substance in diagnosing or detecting Meniere's disease and in
CC      distinguishing this disease from other autoimmune ear diseases.
XX
SQ      Sequence 50000 BP; 17281 A; 9480 C; 8791 G; 14448 T; 0 other;

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Query Match          1.1%; Score 22; DB 21; Length 50000;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1859 AAAATAAATAAATAAAGAAAAGA 1880
        |||||||||||||||||||
DB      45486 aaaaaataataataaagaa 45507

RESULT 8
AAI61659
ID      AAI61659 standard; DNA; 183 BP.
XX
AC      AAI61659;
XX
DT      16-OCT-2001 (first entry)
XX
DE      Soybean 318013 region A3 DNA, SEQ ID NO: 290.
XX
KM      Soybean; antihelminthic; gene therapy; soybean cyst nematode; SCN;
KM      SCN resistance; Rhg1; Rhg4; SCN resistant allele; plant breeding;
KM      240017 region G3; 318013 region A3; 515002 region G2; ds.
XX
OS      Glycine max.
XX
PN      WO200151627-A2.
XX
PD      19-JUL-2001.
XX
PF      05-JAN-2001; 2001MO-US00552.
XX
PR      07-JAN-2000; 2000US-0174880.
XX
PA      (MONS ) MONSANTO CO.
XX
PI      Hauge BM, Wang ML, Parsons JD, Parnell LD;
XX
DR      WPI: 2001-425872/45.
XX
XX      New purified nucleic acid for producing a soybean plant having soybean
PT      cyst nematode resistance and for use in plant breeding programs
XX
PS      Claim 25; Page 1103; 1353pp; English.
XX
CC      The invention relates to nucleic acid molecules from regions of the
CC      soybean genome which are associated with soybean cyst nematode (SCN)
CC      resistance. The nucleic acids are used to transform plants, and can
CC      produce soybean plants having an rhg1 or an Rhg4 SCN resistant allele.
CC      The nucleic acids can be used for investigating rhg1 or Rhg4 haplotypes
CC      of soybean plants and for introgressing SCN resistance or partial SCN
CC      resistance into soybean plants. They can also be used in plant breeding
CC      programmes. The invention also relates to proteins encoded by such
CC      nucleic acid molecules, as well as antibodies capable of recognising
CC      these proteins. The present sequence is a nucleic acid molecule
CC      provided in the specification.
XX
SQ      Sequence 183 BP; 74 A; 12 C; 20 G; 77 T; 0 other;

Query Match          1.0%; Score 21; DB 22; Length 183;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1862 AAAATAAATAAATAAAGAAAAGA 1882
        |||||||||||||||||||
DB      84 aaaaaataataataaagaaaa 104

RESULT 9
AAH04005
ID      AAH04005 standard; cDNA; 885 BP.

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XX AAH04005:
AC
XX 26-JUN-2001 (first entry)
DT
XX Human cDNA clone (5'-primer) SEQ ID NO:840.
DE
XX Human: primer; detection; diagnosis; antisense therapy; gene therapy; ss.
KM
XX Homo sapiens.
OS
XX EPI074617-A2.
EN
XX 07-FEB-2001.
PD
XX 28-JUL-2000; 2000EP-0116126.
PF
XX 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
PA
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
PI
XX WPI; 2001-318749/34.
DR
XX
XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
XX Claim 1; SEQ ID 840; 2537PP + CD ROM; English.
PS
XX
XX CC The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03165 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
XX Sequence 885 BP; 307 A; 145 C; 200 G; 229 T; 4 other;
SQ

```

```

AAQ77883/C
ID AAQ77883 standard; cDNA; 1381 BP.
XX
XX AAQ77883;
AC
XX 06-JUL-1995 (first entry)
DT
XX
XX Neural thread protein AD10-7 cDNA.
DE
XX
XX Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours;
KM malignant astrocytomas; glioblastomas; ss.
XX
XX Rattus rattus.
OS
XX WO9423756-A.
PN
XX 27-OCT-1994.
PD
XX
XX 20-APR-1994; 94WO-US04321.
PF
XX
XX 20-APR-1993; 93US-0050559.
PR
XX
XX (GEHO) GEN HOSPITAL CORP.
PA
XX De LA MONTE SM, Wands JR;
PI
XX WPI; 1994-341497/42.
DR
XX
XX PT Detection of neural thread proteins - to detect sporadic and
PT familial Alzheimer's disease, neuroectodermal tumours, malignant
PT astrocytomas and glioblastomas (Eng).
XX
XX PS Example 4; Fig 16R; 158pp; English.
XX
XX CC AAQ77883 is the AD10-7 neural thread protein (NTP) cDNA. This
CC sequence was used in the development of an antibody dependent
CC method, for the detection of NTPs. This new method could be
CC used to diagnose Alzheimer's disease (differentiating between
CC sporadic and familial), neuroectodermal tumours, malignant
CC astrocytomas and glioblastomas.
XX
XX Sequence 1381 BP; 296 A; 385 C; 301 G; 399 T; 0 other;
SQ

```

```

Query Match 1.0%; Score 21; DB 15; Length 1381;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1858 TAAATAAATAAATAAATAAAG 1878
DB 450 TAAATAAATAAATAAATAAAG 430

```

```

RESULT 11
AAT27765/C
ID AAT27765 standard; cDNA; 1381 BP.
XX
XX AAT27765;
AC
XX
XX 14-NOV-1996 (first entry)
DT
XX
XX AD 10-7 human neural thread protein clone (partial sequence).
DE
XX
XX Neural thread protein; NTP; diagnosis; detection;
KM Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma;
KM monoclonal antibody; binding fragment; ds.
XX
XX Homo sapiens.
OS
XX WO9615272-A1.
PN
XX
XX 23-MAY-1996.
PD
XX
XX

```

RESULT 10

```

PF 14-NOV-1995; 95WO-US1711.1.
XX
XX 14-NOV-1994; 94US-0340426.
XX
XX (GEHO ) GEN HOSPITAL CORP.
PA
XX De LA MONTE S, Wands JR;
XX
XX WPI; 1996-259865/26.
DR
XX
XX Detection of neural thread protein in diagnosis of Alzheimer's
PT disease - also NTP DNA and protein sequences used in gene and
PT anti:sense therapy
PS
XX Example 4c; Figure 16r; 238pp; English.
XX
XX A method for detecting the presence of neural thread protein (NTP)
CC having a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human
CC subject comprises (a) contacting a sample from a human subject that
CC is suspected of containing the NTP with at least one molecule
CC capable of binding to the protein; and (b) detecting any of the
CC molecule bound to the protein. The binding molecule is selected
CC from an antibody free of natural impurities, a monoclonal antibody
CC or a binding fragment of either of these. The method may be used for
CC diagnosing the presence of Alzheimer's disease, neuroectodermal
CC tumours and a malignant astrocytoma in a human. A number of clones
CC of neural thread protein were isolated from healthy 17-18 week old
CC foetal human brain (Hb) 2 year old temporal lobe neocortex and end
CC stage Alzheimer's disease (AD) cerebral cortex. See AAT27753-75.
XX
XX Sequence 1381 BP; 295 A; 385 C; 301 G; 400 T; 0 other;

Query Match 1.0%; Score 21; DB 17; Length 1381;
Best Local Similarity 100.0%; Pred.No.9.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1858 TAAAAAAATATAATATAAAG 1878
DB 450 TAAAAAAATATAATATAAAG 430

RESULT 12
AAT27738/c
ID AAT27738 standard; DNA; 1418 BP.
XX
XX AAT27738;
AC
XX 15-NOV-1996 (first entry)
DT
XX Neural thread protein coding sequence.
DE
XX Neural thread protein; NTP; diagnosis; detection;
KW Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma;
KW monoclonal antibody; binding fragment; ds.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
XX 14..1207
XX CDS /*tag= a
XX /product= Neural thread protein.
XX
XX W09615272-A1.
XX
XX 23-MAY-1996.
XX
XX 14-NOV-1995; 95WO-US1711.1.
XX
XX 14-NOV-1994; 94US-0340426.
XX
XX (GEHO ) GEN HOSPITAL CORP.
XX

```

```

PI De LA MONTE S, Wands JR;
XX
XX WPI; 1996-259865/26.
DR P-PSDB; AAR95913.
XX
XX Detection of neural thread protein in diagnosis of Alzheimer's
PT disease - also NTP DNA and protein sequences used in gene and
PT anti:sense therapy
PS
XX Claim 24; Page 168-170; 238pp; English.
XX
XX A method for detecting the presence of neural thread protein (NTP)
CC having a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human
CC subject comprises (a) contacting a sample from a human subject that
CC is suspected of containing the NTP with at least one molecule
CC capable of binding to the protein; and (b) detecting any of the
CC molecule bound to the protein. The binding molecule is selected
CC from an antibody free of natural impurities, a monoclonal antibody
CC or a binding fragment of either of these. The method may be used for
CC diagnosing the presence of Alzheimer's disease, neuroectodermal
CC tumours and a malignant astrocytoma in a human.
XX
XX Sequence 1418 BP; 302 A; 396 C; 315 G; 405 T; 0 other;

Query Match 1.0%; Score 21; DB 17; Length 1418;
Best Local Similarity 100.0%; Pred.No.9.2;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1858 TAAAAAAATATAATATAAAG 1878
DB 445 TAAAAAAATATAATATAAAG 425

RESULT 13
AAZ97059/c
ID AAZ97059 standard; CDNA; 1423 BP.
XX
XX AAZ97059;
AC
XX 19-APR-2000 (first entry)
DT
XX Human secreted protein gene 41 CDNA clone HSIAC80, SEQ ID NO:51.
DE
XX Human; secreted protein; cancer; tumour; developmental abnormality;
KW foetal deficiency; blood disorder; immune system disorder; inflammation;
KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;
KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;
KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;
KW digestive disorder; endocrine disorder; infection; AIDS; leukaemia;
KW therapy; chromosome 12; ds.
XX
XX Homo sapiens.
OS
XX
XX W09966041-A1.
XX
XX 23-DEC-1999.
XX
XX 15-JUN-1999; 99WO-US13418.
XX
XX 16-JUN-1998; 98US-0089507.
XX 16-JUN-1998; 98US-0089508.
XX 16-JUN-1998; 98US-0089509.
XX 16-JUN-1998; 98US-0089510.
XX 22-JUN-1998; 98US-0090112.
XX 22-JUN-1998; 98US-0090113.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;
PI Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Edner R;
PI Latleur DM, Olsen HS, Shi Y, Moore PA, Komatsu S G;
XX

```

DR WPI: 2000-106100/09.
 DR P-PSDB: AAY66255.
 PT New isolated human genes and the secreted polypeptides they encode,
 PT useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders -
 XX
 PS Claim 1: Page 341: 586pp: English.
 CC AAY67019 to AAY67137 represent 94 isolated human secreted protein genes.
 CC AAY6615 to AAY6633 are the secreted proteins encoded by the 94 human
 CC genes. This sequence represents a fragment of one of the human secreted
 CC proteins. The genes and their corresponding secreted polypeptides are
 CC useful for preventing, treating or ameliorating medical conditions,
 CC e.g., by protein or gene therapy. Also pathological conditions can be
 CC diagnosed by determining the amount of the new polypeptides in a sample
 CC or by determining the presence of mutations in the new genes. Specific
 CC uses are described for each of the 94 genes, based on which tissues they
 CC are most highly expressed in, and include developing products for the
 CC diagnosis or treatment of cancer, tumours, developmental abnormalities
 CC and foetal deficiencies, blood disorders, diseases of the immune system,
 CC autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
 CC disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
 CC disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
 CC disorders, digestive/endocrine disorders, infections and AIDS. The
 CC polypeptides are also useful for identifying their binding partners.
 CC The sequences shown in AAY66334 to AAY66585 represent fragments of the
 CC secreted proteins.
 CC
 SO Sequence 1423 BP; 489 A; 215 C; 195 G; 524 T; 0 other;
 Query Match 1.0%; Score 21; DB 21; Length 1423;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 635 AAAAATTAAATTTTATTC 655
 ||||||||||||||||||
 DB 523 AAAAATTAAATTTTATTC 503
 RESULT 14
 ID AAF18279 standard; DNA; 1682 BP.
 XX AAF18279;
 AC
 DT 14-MAR-2001 (first entry)
 DE
 XX Lung cancer associated polynucleotide sequence SEQ ID 298.
 KW Human: lung cancer associated protein; neuroprotective; cytostatic;
 KW cardiactive; immunomodulatory; muscular active; vulnarary;
 KW gastrointestinal; nephrotropic; antinefactive; gynecological;
 KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
 KW proliferative disorder; wound healing; infectious disease; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200055180-A2.
 PD 21-SEP-2000.
 XX
 PF 08-MAR-2000; 2000WO-US05918.
 XX
 PR 12-MAR-1999; 99US-0124270.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 PI Ruben SM;
 XX
 WPI: 2000-587514/55.

DR P-PSDB: AAB58403.
 XX
 PT Lung cancer associated gene sequences, referred to as lung cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as lung cancer -
 XX
 PS Claim 1: Page 757: 1425pp: English.
 CC Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
 CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
 CC associated proteins and polynucleotide sequences, their agonists, and
 CC antagonists may have neuroprotective, cytostatic, cardiactive,
 CC immunomodulatory; muscular active general; vulnarary; gastrointestinal
 CC general; nephrotropic; antinefactive; gynecological; or antibacterial
 CC activity. The invention also includes antibodies specific for the
 CC protein or polynucleotide sequences. The lung cancer associated
 CC polynucleotide sequences may be used for detection of lung cancer,
 CC chromosome identification, as chromosome markers, and for numerous other
 CC diagnostic or research purposes. The proteins may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders. The proteins may also be used in the treatment of wounds and
 CC infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and
 CC peptide AAB58349 are used in the course of the invention for the
 CC identification and characterisation of the polynucleotide and protein
 CC sequences.
 CC
 SO Sequence 1682 BP; 383 A; 551 C; 430 G; 310 T; 8 other;
 Query Match 1.0%; Score 21; DB 21; Length 1682;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1857 GTAAAAAATTAATTAATAA 1877
 ||||||||||||||||||
 DB 1537 gtaaaaaataataataaaaa 1557
 RESULT 15
 ID AA256739/C standard; CDNA; 1737 BP.
 XX AA256739;
 AC
 DT 23-MAR-2000 (first entry)
 DE
 XX Human transmembrane protein HTMPN-42 encoding CDNA.
 KW Human: transmembrane protein; HTMPN; diagnosis; immunospecific;
 KW antiproliferative; neuroprotective; immune disorder;
 KW reproductive disorder; smooth muscle disorder; neurological disorder;
 KW gastrointestinal disorder; developmental disorder;
 KW cell proliferative disorder; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9961471-A2.
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11904.
 XX
 PR 29-MAY-1998; 98US-0087260.
 PR 02-JUL-1998; 98US-0091674.
 PR 02-OCT-1998; 98US-0102954.
 PR 24-NOV-1998; 98US-0109869.
 XX
 PA (INCY-) INCYTE PHARM INC.
 PA
 XX Tang YT, Ial P, Hillman JL, Yue H, Guegler KJ, Corley NC;
 PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR;
 PI Au-Young J;

XX MPI: 2000-072605/06.
 DR F-PSDB: AA57918.

XX
 PT Proteins, polynucleotides, vectors, host cells and antibodies used to
 PT diagnose, treat or prevent immune, reproductive, smooth muscle,
 PT neurological, gastrointestinal, developmental and cell proliferative
 PT disorders -

XX
 PS Claim 9; Page 205; 229pp; English.

XX
 CC AA256698 to AA256776 encode AA57877 to AA57955 which represent human
 CC transmembrane proteins designated HTPN-1 to HTPN-79, respectively.
 CC The transmembrane protein have immunospecific, antiproliferative and
 CC neuroprotective activities. The human transmembrane proteins,
 CC polynucleotides encoding them and other compositions and methods from
 CC the present invention, can be used for the diagnosis, treatment or
 CC prevention of immune, reproductive, smooth muscle, neurological, the
 CC gastrointestinal, developmental and cell proliferative disorders. The
 CC HTPN's can be used to treat or prevent disorders associated with a
 CC decreased expression or activity of HTPN.

XX
 SQ Sequence 1737 BP; 578 A; 249 C; 246 G; 664 T; 0 other;

Query Match

Best Local Similarity 1.08; Score 21; DB 21; Length 1737;
 Pred. No. 9.2;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 635 AAAAATTTAAATTTATTC 655
 ||||||||||||||||
 DB 497 AAAAATTTAAATTTATTC 477

Search completed: April 16, 2002, 19:36:41
 Job time: 10196 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2002, 16:46:15 ; Search time 1100.43 seconds

(without alignments)
20409.001 Million cell updates/sec

Title: US-09-636-826-1

Perfect score: 2090

Sequence: 1 GATATCACACATTCGTCAT.....TCGGCTTCTCGGTGCTGCT 2090

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 11351937 seqs, 5372889281 residues

Word size: 0

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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2: em_esthm:*

3: em_estlm:*

4: em_estom:*

5: em_estpl:*

6: em_estba:*

7: em_estro:*

8: em_estov:*

9: em_htc:*

10: gb_estl:*

11: gb_estz:*

12: gb_htc:*

13: gb_hss:*

14: em_gss_fun:*

15: em_gss_hum:*

16: em_gss_jay:*

17: em_gss_pln:*

18: em_gss_pro:*

19: em_gss_rtd:*

20: em_gss_vrt:*

21: em_gss_other:*

* Pred. No. is the number of results predicted by chance to have a
* score greater than or equal to the score of the result being printed,
* and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	32	1.5	456 10	AM266586 L0-1455T3
2	32	1.5	496 10	AM266151 L30-2844T
3	32	1.5	548 10	BE131353 L48-1327T
4	32	1.5	564 10	AA962891 L30-421T3
5	32	1.5	568 10	AM266784 L48-122T3
6	32	1.5	569 10	BE037420 MP20H01 M
7	32	1.5	684 11	BF479545 L48-3229T
8	32	1.5	689 11	BF479194 L48-2850T
9	32	1.5	702 10	BE130820 L48-1763T
10	32	1.5	717 11	BF479434 L48-3109T
11	32	1.5	762 10	BE131075 L48-1025T
12	32	1.5	815 10	BE036727 MP04D04 M

13	32	1.5	940 10	BE036821 MP06H04 M
14	31	1.5	911 10	BE034072 M
15	31	1.5	307 11	BE216792 M
16	26	1.2	456 11	D32461
17	26	1.2	677 10	AU213676
18	25	1.2	894 11	BF675049
19	24	1.1	590 13	AQ423092 CTRB-E1-
20	24	1.1	800 13	A2528823
21	24	1.1	852 13	A2683403
22	24	1.1	890 13	A2687945
23	23	1.1	446 10	AL586234
24	23	1.1	467 13	A2804361
25	23	1.1	546 11	BF646364
26	23	1.1	573 13	A2114192
27	23	1.1	632 11	BF295656
28	23	1.1	649 11	BF298841
29	23	1.1	669 13	A2524829
30	23	1.1	683 13	A2577684
31	23	1.1	701 13	AG019716
32	23	1.1	840 13	CNS01EFP
33	22	1.1	208 11	R75193
34	22	1.1	241 10	BS592256
35	22	1.1	308 10	AU062037
36	22	1.1	333 10	AY094649
37	22	1.1	438 10	AM840674
38	22	1.1	489 11	BG347359
39	22	1.1	511 11	C23717
40	22	1.1	518 10	AU052004
41	22	1.1	543 10	AU155621
42	22	1.1	565 13	A2840399
43	22	1.1	574 10	A1641746
44	22	1.1	611 13	BH114399
45	22	1.1	624 13	A2502227

ALIGNMENTS

RESULT 1

AM266586

LOCUS

DEFINITION

10-1455T3 Ice plant Lambda uni-zap XR expression library, 0 hours

NaCl treatment Mesembryanthemum crystallinum cDNA clone 10-1455 5',

mRNA sequence.

ACCESSION

AM266586

VERSION

AM266586.1

KEYWORDS

GT:6647072

ORGANISM

common ice plant.

Mesembryanthemum crystallinum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;

Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.

1 (bases 1 to 456)

Cushman, J.C.

An expressed sequence tag database for the common ice plant,

Mesembryanthemum crystallinum

Unpublished (1997)

Contact: Cushman JC

Department of Biochemistry

University of Nevada

MS200, Reno, NV 89557-0014, USA

Tel: 775-784-1918

Fax: 775-784-1650

Email: jcushman@unr.edu

PCR Primers

FORWARD: T7

BACKWARD: T3

Plate: 10-15

Seq primer: T3

High quality sequence stop: 350.

Location/Qualifiers

1..456

/organism="Mesembryanthemum crystallinum"

/db_xref="taxon:3544"
/clone_lib="ice plant lambda uni-zap XR expression library"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 79 a 102 c 117 g 158 t
ORIGIN

Query Match 1.5%; Score 32; DB 10; Length 456;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2046 AACGGCGATGAACGGCGCGTCTTCGGCTT 2077
|||||
Db 79 AACGGCGATGAACGGCGCGTCTTCGGCTT 110
|||||

RESULT 2
AW266151 496 bp mRNA EST 20-FEB-2001
LOCUS L30-2844T3 Ice plant lambda Uni-zap XR expression library, 30 hours
DEFINITION NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-2844
5', mRNA sequence.
ACCESSION AM266151 GI:6644838
VERSION AM266151.1
KEYWORDS EST.
SOURCE Common ice plant.
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllaceae; Alstrocheae; Mesembryanthemum.
1 (bases 1 to 496)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel.: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMERS
FORWARD: T7
BACKWARD: T3
Plate: L30-29 row: D column: 12
Seq primer: T3
High quality sequence stop: 350.
Location/Qualifiers
1. 496
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone_lib="L30-2844"
/clone_lib="ice plant lambda Uni-zap XR expression library"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 107 a 110 c 107 g 172 t
ORIGIN

Query Match 1.5%; Score 32; DB 10; Length 496;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2046 AACGGCGATGAACGGCGCGTCTTCGGCTT 2077

|||||
Db 355 AACGGCGATGAACGGCGCGTCTTCGGCTT 386
|||||

RESULT 3
BE131353 548 bp mRNA EST 20-FEB-2001
LOCUS L48-1327T3 Ice plant lambda Uni-zap XR expression library, 48 hours
DEFINITION NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-1327,
mRNA sequence.
ACCESSION BE131353 GI:8578716
VERSION BE131353.1
KEYWORDS EST.
SOURCE Common ice plant.
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllaceae; Alstrocheae; Mesembryanthemum.
1 (bases 1 to 548)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel.: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR PRIMERS
FORWARD: T7
BACKWARD: T3
Plate: L48-14 row: C column: 3
Seq primer: T3
High quality sequence stop: 350
POLYA=No.
Location/Qualifiers
1. 548
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone_lib="L48-1327"
/clone_lib="ice plant lambda Uni-zap XR expression library"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-zap XR, Bluescript SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 89 a 126 c 137 g 196 t
ORIGIN

Query Match 1.5%; Score 32; DB 10; Length 548;
Best Local Similarity 100.0%; Pred. No. 0.0085;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2046 AACGGCGATGAACGGCGCGTCTTCGGCTT 2077
|||||
Db 85 AACGGCGATGAACGGCGCGTCTTCGGCTT 116
|||||

RESULT 4
AA962891 564 bp mRNA EST 20-FEB-2001
LOCUS L30-421T3 Ice plant lambda Uni-zap XR expression library, 30 hours
DEFINITION NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-421 5',
similar to vacuolar H⁺-ATPase, 16 kDa proteolipid subunit, mRNA
sequence.
ACCESSION AA962891
VERSION AA962891.1 GI:3136364
KEYWORDS EST.
SOURCE Common ice plant.
ORGANISM Mesembryanthemum crystallinum

REFERENCE
AUTHORS
TITLE
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum

JOURNAL

COMMENT
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7
BACKWARD: T3
Plate: L30-5 row: C column: 1
Seq primer: T3
High quality sequence stop: 350.
Location/Qualifiers

FEATURES

source
1..564
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone="130-421"
/clone_1lb="ice plant Lambda Uni-zap XR expression library
30 hours NaCl treatment"
/tissue_type="leaf, 30 h 0.4M NaCl"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

BASE COUNT

97 a 138 c 132 g 197 t

ORIGIN

Query Match 1.5%; Score 32; DB 10; Length 564;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AACGGCGATGAACGGCGCGCTTCTCGGCTT 2077
DB 128 AACGGCGATGAACGGCGCGCTTCTCGGCTT 159

RESULT 5

LOCUS
DEFINITION
AM266784 568 bp mRNA EST 20-FEB-2001
L48-122T3 Ice plant Lambda Uni-zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-122 5',
mRNA sequence.

ACCESSION
VERSION
KEYWORDS
AM266784
AM266784.1 GI:6647219
EST.

SOURCE

ORGANISM
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Alstroceae; Mesembryanthemum.
1 (bases 1 to 568)
Cushman, J.C.
An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
Unpublished (1997)

REFERENCE

AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7

BACKWARD: T3
Plate: L48-2 row: C column: 2
Seq primer: T3
High quality sequence stop: 350.
Location/Qualifiers

FEATURES

source
1..568
/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone="148-122"
/clone_1lb="ice plant Lambda Uni-zap XR expression library
48 hours NaCl treatment"
/tissue_type="leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"

BASE COUNT

98 a 133 c 141 g 196 t

ORIGIN

Query Match 1.5%; Score 32; DB 10; Length 568;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AACGGCGATGAACGGCGCGCTTCTCGGCTT 2077
DB 87 AACGGCGATGAACGGCGCGCTTCTCGGCTT 118

RESULT 6

LOCUS
DEFINITION
BE037420 569 bp mRNA EST 07-JUN-2000
MP20H01 MP Mesembryanthemum crystallinum cDNA 5' similar to
vacuolar atp synthase 16 kd proteolipid subunit, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
BE037420
BE037420.1 GI:8332436
EST.

SOURCE

ORGANISM
Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Alstroceae; Mesembryanthemum.
1 (bases 1 to 569)
Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira,
H., Kawasaki, S., McCollough, A., Michalowski, C.B., Palacios, C.,
Scara, G., Wheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished (2000)

TITLE

JOURNAL
COMMENT
Contact: Michalowski, C.B.
University of Arizona
Bio Sciences West Room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cdm@u.arizona.edu
Insert Length: 1 Std Error: 0.00.
Location/Qualifiers

FEATURES

source
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/organism="Mesembryanthemum crystallinum"
/db_xref="taxon:3544"
/clone_1lb="MP"
/tissue_type="apical meristem and leaf primordia"
/dev_stage="6 weeks"
/note="3 d 500mM NaCl"

BASE COUNT

110 a 119 c 149 g 191 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AACGGCGATGAACGGCGCGCTTCTCGGCTT 2077
DB 55 AACGGCGATGAACGGCGCGCTTCTCGGCTT 86

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RESULT 7
LOCUS BF479545 684 bp mRNA EST 20-FEB-2001
DEFINITION L48-3229t3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-3229
5', mRNA sequence.
ACCESSION BF479545
VERSION BF479545.1 GI:11550372
KEYWORDS EST.
SOURCE Common ice plant.
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Alstroceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 684)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
JOURNAL Mesembryanthemum crystallinum
COMMENT Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7
BACKWARD: T3
Plate: L48-29 row: E column: 2
Seq primer: T3
High quality sequence stop: 350
POLYA-No.

FEATURES
source Location/Qualifiers
1..684
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/db_xref="taxon:3544"
/clone="L48-3229"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library"
, 48 hours NaCl treatment"
/tissue_type="Leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
BASE COUNT 123 a 162 c 165 g 234 t
ORIGIN

Query Match 1.5%; Score 32; DB 11; Length 684;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AACGGCGATGAACGGCGCGCTCTCGGCTT 2077
|||||
Db 89 AACGGCGATGAACGGCGCGCTCTCGGCTT 120

RESULT 8
LOCUS BF479194 689 bp mRNA EST 20-FEB-2001
DEFINITION L48-2850t3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-2850
5', mRNA sequence.
ACCESSION BF479194
VERSION BF479194.1 GI:11550021
KEYWORDS EST.
SOURCE Common ice plant.
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Alstroceae; Mesembryanthemum.

REFERENCE 1 (bases 1 to 689)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
JOURNAL Mesembryanthemum crystallinum
COMMENT Unpublished (1997)
Contact: Cushman JC
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Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7
BACKWARD: T3
Plate: L48-29 row: E column: 2
Seq primer: T3
High quality sequence stop: 350
POLYA-No.

FEATURES
source Location/Qualifiers
1..689
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/db_xref="taxon:3544"
/clone="L48-2850"
/clone_lib="Ice plant Lambda Uni-Zap XR expression library"
, 48 hours NaCl treatment"
/tissue_type="Leaf, 48 h 0.4M NaCl"
/dev_stage="Six week old"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
BASE COUNT 123 a 164 c 160 g 242 t
ORIGIN

Query Match 1.5%; Score 32; DB 11; Length 689;
Best Local Similarity 100.0%; Pred. No. 0.0078;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AACGGCGATGAACGGCGCGCTCTCGGCTT 2077
|||||
Db 103 AACGGCGATGAACGGCGCGCTCTCGGCTT 134

RESULT 9
LOCUS BE130820 702 bp mRNA EST 20-FEB-2001
DEFINITION L48-1763t3 Ice plant Lambda Uni-Zap XR expression library, 48 hours
NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-1763
5', mRNA sequence.
ACCESSION BE130820
VERSION BE130820.1 GI:8578209
KEYWORDS EST.
SOURCE Common ice plant.
ORGANISM Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllales; Alstroceae; Mesembryanthemum.
REFERENCE 1 (bases 1 to 702)
AUTHORS Cushman, J.C.
TITLE An expressed sequence tag database for the common ice plant,
JOURNAL Mesembryanthemum crystallinum
COMMENT Unpublished (1997)
Contact: Cushman JC
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Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T7
BACKWARD: T3
Plate: L48-18 row: F column: 3

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Seq primer: T3

High quality sequence stop: 350

FEATURES

SOURCE

Location/Qualifiers

1..702

/organism="Mesembryanthemum crystallinum"

/db_xref="taxon:3544"

/clone_lib="ice plant Lambda Uni-Zap XR expression library

, 48 hours NaCl treatment"

/tissue_type="leaf, 48 h 0.4M NaCl"

/dev_stage="Six week old"

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:

EcoRI; Site_2: XhoI"

BASE COUNT

130 a 157 c 170 g 245 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 32; DB 10; Length 702;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2046 AACGGGATGAACGGCCGCTTCCTCGGCTT 2077

Db

74 AACGGGATGAACGGCCGCTTCCTCGGCTT 105

RESULT 10

BF479434

LOCUS

BF479434 717 bp mRNA EST 20-FEB-2001
L48-3109T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours

DEFINITION

NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-3109

ACCESSION

BF479434

VERSION

BF479434.1 GI:11550261

KEYWORDS

EST.

SOURCE

common ice plant.

ORGANISM

Mesembryanthemum crystallinum

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AUTHORS

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

TITLE

Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.

JOURNAL

1 (bases 1 to 717)

COMMENT

An expressed sequence tag database for the common ice plant,

JOURNAL

Mesembryanthemum crystallinum

COMMENT

Unpublished (1997)

JOURNAL

Contact: Cushman JC

COMMENT

Department of Biochemistry

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COMMENT

Email: jcushman@unr.edu

COMMENT

PCR Primers

COMMENT

FORWARD: T7

COMMENT

BACKWARD: T3

COMMENT

Plate: L48-32

COMMENT

Seq primer: T3

COMMENT

High quality sequence stop: 350

COMMENT

POLYA-No.

FEATURES

Location/Qualifiers

SOURCE

1..717

ORGANISM

/organism="Mesembryanthemum crystallinum"

DB

/db_xref="taxon:3544"

LOCUS

/clone_lib="ice plant Lambda Uni-Zap XR expression library

DEFINITION

, 48 hours NaCl treatment"

TISSUE

/tissue_type="leaf, 48 h 0.4M NaCl"

DEV_STAGE

/dev_stage="Six week old"

NOTE

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:

Query Match

1.5%; Score 32; DB 11; Length 717;

Best Local Similarity 100.0%; Pred. No. 0.0077;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AACGGGATGAACGGCCGCTTCCTCGGCTT 2077

Db 149 AACGGGATGAACGGCCGCTTCCTCGGCTT 180

RESULT 11

BE131075

LOCUS

BE131075 762 bp mRNA EST 20-FEB-2001

DEFINITION

L48-1025T3 Ice plant Lambda Uni-Zap XR expression library, 48 hours

ACCESSION

L48-1025T3

VERSION

NaCl treatment Mesembryanthemum crystallinum cDNA clone L48-1025

KEYWORDS

5', mRNA sequence.

SOURCE

BE131075.1 GI:8578438

ORGANISM

EST.

REFERENCE

common ice plant.

AUTHORS

Mesembryanthemum crystallinum

TITLE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

JOURNAL

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

COMMENT

Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.

COMMENT

1 (bases 1 to 762)

COMMENT

Cushman, J.C.

COMMENT

An expressed sequence tag database for the common ice plant,

COMMENT

Mesembryanthemum crystallinum

COMMENT

Unpublished (1997)

COMMENT

Contact: Cushman JC

COMMENT

Department of Biochemistry

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University of Nevada

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MS200, Reno, NV 89557-0014, USA

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Tel: 775-784-1918

COMMENT

Fax: 775-784-1650

COMMENT

Email: jcushman@unr.edu

COMMENT

PCR Primers

COMMENT

FORWARD: T7

COMMENT

BACKWARD: T3

COMMENT

Plate: L48-11

COMMENT

Seq primer: T3

COMMENT

High quality sequence stop: 350

COMMENT

POLYA-No.

FEATURES

Location/Qualifiers

SOURCE

1..762

ORGANISM

/organism="Mesembryanthemum crystallinum"

DB

/db_xref="taxon:3544"

LOCUS

/clone_lib="ice plant Lambda Uni-Zap XR expression library

DEFINITION

, 48 hours NaCl treatment"

TISSUE

/tissue_type="leaf, 48 h 0.4M NaCl"

DEV_STAGE

/dev_stage="Six week old"

NOTE

/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:

EcoRI; Site_2: XhoI"

BASE COUNT

151 a 163 c 209 g 239 t

ORIGIN

Query Match

1.5%; Score 32; DB 10; Length 762;

Best Local Similarity

100.0%; Pred. No. 0.0075;

Matches

32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2046 AACGGGATGAACGGCCGCTTCCTCGGCTT 2077

Db

47 AACGGGATGAACGGCCGCTTCCTCGGCTT 78

RESULT 12

BE036727

LOCUS

BE036727 815 bp mRNA EST 07-JUN-2000

DEFINITION

MP04D04 MP Mesembryanthemum crystallinum cDNA 5' similar to

vacuolar atp synthase 16 kd proteolipid subunit, mRNA sequence.

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ACCESSION      BE036727.1  GI:8331736
VERSION        BE036727.1
KEYWORDS       common ice plant.
SOURCE         Mesembryanthemum crystallinum
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
REFERENCE      1 (bases 1 to 815)
AUTHORS        Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira,
                H., Kawasaki, S., McColough, A., Michalowski, C.B., Palacio, C.,
                Scara, G., Wheeler, M. and Zepeda, G.R.
                Functional Genomics of Plant Stress Tolerance
                Unpublished (2000)
TITLE          Contact: Michalowski, C.B.
JOURNAL        University of Arizona
COMMENT        Bio Sciences West room 513, Tucson, AZ 85721, USA
                Tel: 520-621-7982
                Fax: 520-621-1697
                Email: cbm@u.arizona.edu
                An open reading frame exists.
FEATURES
SOURCE         1. 815
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                /db_xref="taxon:3544"
                /clone_lib="MP"
                /tissue_type="apical meristem and leaf primordia"
                /dev_stage="6 weeks"
                /note="3 d 500mM NaCl"
BASE COUNT     160 a 183 c 197 g 275 t
ORIGIN
Query Match    1.5%; Score 32; DB 10; Length 815;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2046 AACGGCGATGAACGGCGCGCTTCTTGGCCTT 2077
|||||
Db 84 AACGGCGATGAACGGCGCGCTTCTTGGCCTT 115

RESULT 13
BE036821      940 bp  mRNA  EST 07-JUN-2000
LOCUS        MP06H04 MP Mesembryanthemum crystallinum cDNA 5' similar to
DEFINITION   vacuolar atp synthase, mRNA sequence.
ACCESSION    BE036821
VERSION      BE036821.1  GI:8331837
KEYWORDS     EST.
SOURCE       common ice plant.
ORGANISM     Mesembryanthemum crystallinum
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
REFERENCE    1 (bases 1 to 940)
AUTHORS      Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira,
                H., Kawasaki, S., McColough, A., Michalowski, C.B., Palacio, C.,
                Scara, G., Wheeler, M. and Zepeda, G.R.
                Functional Genomics of Plant Stress Tolerance
                Unpublished (2000)
TITLE        Contact: Michalowski, C.B.
JOURNAL      University of Arizona
COMMENT      Bio Sciences West room 513, Tucson, AZ 85721, USA
                Tel: 520-621-7982
                Fax: 520-621-1697
                Email: cbm@u.arizona.edu
                An open reading frame exists.
FEATURES
SOURCE         1. 940
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                /db_xref="taxon:3544"
                /clone_lib="MP"

ACCESSION      BE034072      911 bp  mRNA  EST 07-JUN-2000
VERSION        BE034072
DEFINITION     MG04G07 MG Mesembryanthemum crystallinum cDNA 5' similar to
                h+transporing atpase, mRNA sequence.
ACCESSION      BE034072.1  GI:8329081
KEYWORDS       EST.
SOURCE         common ice plant.
ORGANISM       Mesembryanthemum crystallinum
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                Caryophyllidae; Caryophyllales; Alzooceae; Mesembryanthemum.
REFERENCE      1 (bases 1 to 911)
AUTHORS        Bohner, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferreira,
                H., Kawasaki, S., McColough, A., Michalowski, C.B., Palacio, C.,
                Scara, G., Wheeler, M. and Zepeda, G.R.
                Functional Genomics of Plant Stress Tolerance
                Unpublished (2000)
TITLE          Contact: Michalowski, C.B.
JOURNAL        University of Arizona
COMMENT        Bio Sciences West room 513, Tucson, AZ 85721, USA
                Tel: 520-621-7982
                Fax: 520-621-1697
                Email: cbm@u.arizona.edu.
FEATURES
SOURCE         1. 911
                /organism="Mesembryanthemum crystallinum"
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                /clone_lib="MG"
                /tissue_type="roots"
                /dev_stage="5-6 weeks"
                /note="grown in hydroponics, stress 400 mM NaCl (in 0.5
                Hoagland's), 30 h stress"
BASE COUNT     151 a 258 c 236 g 259 t 7 others
ORIGIN
Query Match    1.5%; Score 31; DB 10; Length 911;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2047 ACGGCGATGAACGGCGCGCTTCTTGGCCTT 2077
|||||
Db 46 ACGGCGATGAACGGCGCGCTTCTTGGCCTT 76

RESULT 15
BG216792/c    307 bp  tRNA  EST 21-APR-2001
LOCUS        RST36487 Atcherys Rage Library Homo sapiens cDNA, mRNA sequence.
DEFINITION   BG216792
ACCESSION    BG216792.1  GI:13742813
VERSION      BG216792.1
KEYWORDS     EST.
SOURCE       human.
ORGANISM     Homo sapiens
                Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

```

REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 307)
Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Krasnoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
Velooso,N., Hess,J., Cochran,K., Lo,K., Offenbacher,J., Danzig,J.
and Ducar,M.

TITLE

Creation of Genome-wide Protein Expression Libraries using Random
Activation of Gene Expression

JOURNAL

Nat. Biotechnol. 19 (5), 440 (2001) In press

COMMENT

Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com

FEATURES

source

1..307
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

BASE COUNT
ORIGIN

108 a 39 c 56 g 104 t

Query Match

Best Local Similarity 1.3%; Score 28; DB 11; Length 307;
Pred. No. 0.49;

Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 537 AAAATTATTTAATATTAATGAAT 564

Db 287 AAAATTATTTAATATTAATGAAT 260

Search completed: April 16, 2002, 19:32:40
Job time: 9985 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 16, 2002, 16:32:25 ; Search time 52.84 Seconds
(without alignments)
8957,968 Million cell updates/sec

Title: US-09-636-826-1

Perfect score: 2090
Sequence: 1 GATATCAGACATTCGTCAT.....TCGCGTTCTCGGCTGCTGCT 2090

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 351203 seqs, 113238999 residues

Word size : 0

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued_Patents_NA.*
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2: /cgn2.6/ptodata/2/ina/5B.COMB.seq.*
3: /cgn2.6/ptodata/2/ina/6A.COMB.seq.*
4: /cgn2.6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2.6/ptodata/2/ina/PTC05.COMB.seq.*
6: /cgn2.6/ptodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	1.1	5590	4 US-09-050-159-129	Sequence 129, App
2	21	1.0	1381	2 US-08-454-557C-49	Sequence 49, Appl
3	21	1.0	1381	2 US-08-346-426D-49	Sequence 49, Appl
4	21	1.0	1381	2 US-08-450-673C-49	Sequence 49, Appl
5	21	1.0	1381	2 PCT-US95-17111A-49	Sequence 49, Appl
6	21	1.0	1418	5 PCT-US95-17111A-120	Sequence 120, App
7	21	1.0	1442	2 US-08-454-557C-120	Sequence 120, App
8	21	1.0	1442	2 US-08-340-426D-120	Sequence 120, App
9	21	1.0	1442	2 US-08-450-673C-120	Sequence 120, App
10	20	1.0	404	1 US-08-594-031-154	Sequence 154, App
11	20	1.0	634	1 US-08-450-065-1	Sequence 1, Appl
12	20	1.0	634	1 US-08-450-595-1	Sequence 1, Appl
13	20	1.0	2733	1 US-08-676-967-3	Sequence 3, Appl
14	20	1.0	2733	1 US-08-676-974-3	Sequence 3, Appl
15	20	1.0	2733	2 US-09-058-487-3	Sequence 3, Appl
16	20	1.0	4233	2 US-09-120-513-1	Sequence 1, Appl
17	20	1.0	4233	4 US-09-450-105-1	Sequence 1, Appl
18	19	0.9	1229	2 US-08-975-316-85	Sequence 85, Appl
19	19	0.9	1959	1 US-08-344-411A-3	Sequence 3, Appl
20	19	0.9	1959	5 PCT-US94-12883-4	Sequence 4, Appl
21	19	0.9	1982	3 US-08-747-221B-13	Sequence 13, Appl
22	19	0.9	1982	4 US-08-747-221B-15	Sequence 15, Appl
23	19	0.9	1982	4 US-09-005-051-13	Sequence 13, Appl
24	19	0.9	1982	4 US-09-005-051-15	Sequence 15, Appl
25	19	0.9	2144	3 US-08-747-221B-57	Sequence 57, Appl
26	19	0.9	2144	3 US-08-747-221B-59	Sequence 59, Appl
27	19	0.9	2144	4 US-09-005-051-57	Sequence 57, Appl

28	19	0.9	2144	4 US-09-005-051-59	Sequence 59, Appl
29	19	0.9	3528	4 US-08-984-320-2	Sequence 2, Appl
30	19	0.9	3528	4 US-08-487-087A-2	Sequence 2, Appl
31	19	0.9	4383	6 5175095-4	Patent No.5175095
32	19	0.9	12565	4 US-09-345-217-3	Sequence 3, Appl
33	19	0.9	19124	2 US-08-487-826B-13	Sequence 13, Appl
34	18	0.9	69	1 US-08-146-421-2	Sequence 2, Appl
35	18	0.9	301	4 US-09-053-021-3	Sequence 3, Appl
36	18	0.9	345	4 US-09-053-021-8	Sequence 8, Appl
37	18	0.9	1301	4 US-08-804-166-7	Sequence 7, Appl
38	18	0.9	1301	4 US-08-910-991-7	Sequence 7, Appl
39	18	0.9	1442	1 US-08-468-763-18	Sequence 18, Appl
40	18	0.9	1442	2 US-08-393-996A-18	Sequence 18, Appl
41	18	0.9	1560	1 US-08-194-180-2	Sequence 2, Appl
42	18	0.9	1784	3 US-08-991-426-1	Sequence 1, Appl
43	18	0.9	1784	3 US-09-143-470-1	Sequence 1, Appl
44	18	0.9	1934	4 US-08-776-844-1	Sequence 1, Appl
45	18	0.9	2422	4 US-08-952-365-7	Sequence 7, Appl

ALIGNMENTS

```

RESULT 1
US-09-050-159-129
; Sequence 129, Application US/09050159A
; Patent No. 6197505
; GENERAL INFORMATION:
; APPLICANT: No. 6197505berg, Lelf T
; APPLICANT: Andersson, Maria K
; APPLICANT: Linstrom, Per H
; TITLE OF INVENTION: METHODS FOR ASSESSING CARDIOVASCULAR STATUS AND
; FILE REFERENCE: 1248/ID042
; CURRENT FILING DATE: 1998-03-27
; EARLIER APPLICATION NUMBER: 60/042,930
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 129
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Angiotensin I converting enzyme, 5' region
US-09-050-159-129

Query Match 1.1%; Score 22; DB 4; Length 5590;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1860 AAAAAATTAATTAAGGAA 1861
Db 842 aaaaaataataataaagaa 863

RESULT 2
US-08-454-557C-49/c
; Sequence 49, Application US/08454557C
; Patent No. 5830670
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.

```

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; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,557C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2500
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-454-557C-49

Query Match          1.0%; Score 21; DB 2; Length 1381;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1858 TAAAAAAATTAATAATAAG 1878
DQ 450 TAAAAAAATTAATAATAAG 430

RESULT
US-08-340-426D-49/C
; Sequence 49, Application US/08340426D
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/340,426D
; FILING DATE: 14-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2500
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid

```

```

; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-340-426D-49

Query Match          1.0%; Score 21; DB 2; Length 1381;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1858 TAAAAAAATTAATAATAAG 1878
DQ 450 TAAAAAAATTAATAATAAG 430

RESULT
US-08-450-673C-49/C
; Sequence 49, Application US/08450673C
; Patent No. 5948688
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
; TITLE OF INVENTION: of Alzheimer's Disease
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,673C
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, Steven R.
; REGISTRATION NUMBER: 36,203
; REFERENCE/DOCKET NUMBER: 0609.3840004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2540
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1381 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-450-673C-49

Query Match          1.0%; Score 21; DB 2; Length 1381;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1858 TAAAAAAATTAATAATAAG 1878
DQ 450 TAAAAAAATTAATAATAAG 430

RESULT
PCT-US95-17111A-49/C
; Sequence 49, Application PC/TUS9517111A
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; TITLE OF INVENTION: Neural Thread Protein Gene Expression and
; TITLE OF INVENTION: Detection of Alzheimer's Disease

```

NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 1381 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
PCT-US95-17111A-49

Query Match 1.0%; Score 21; DB 5; Length 1381;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1858 TAAATAAATAAATAAATAAG 1878
|||||
DB 450 TAAATAAATAAATAAATAAG 430

RESULT 6
PCT-US95-17111A-120/C
Sequence 120, Application PC/TUS9517111A
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994

ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 1418 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
FEATURE:
NAME/KEY: CDS
LOCATION: 14..1418
PCT-US95-17111A-120

Query Match 1.0%; Score 21; DB 5; Length 1418;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1858 TAAATAAATAAATAAATAAG 1878
|||||
DB 445 TAAATAAATAAATAAATAAG 425

RESULT 7
US-08-454-557C-120/C
Sequence 120, Application US/08454557C
Patent No. 5830670
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 120:
SEQUENCE CHARACTERISTICS:
LENGTH: 1442 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 15..1139
US-08-454-557C-120

Query Match 1.0%; Score 21; DB 2; Length 1442;

Best Local Similarity 100.0%; Pred No. 4.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1858 TAAAAAAATATAATAAAG 1878

DB 446 TAAAAAAATATAATAAAG 426

RESULT 8

US-08-340-426D-120/C

; Sequence 120; Application US/08340426D

; Patent No. 5948634

; GENERAL INFORMATION:

; APPLICANT: de la Monte, Suzanne

; APPLICANT: Wands, Jack R.

; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

; TITLE OF INVENTION: of Alzheimer's Disease

; NUMBER OF SEQUENCES: 121

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/340,426D

; FILING DATE: 14-NOV-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, Steven R.

; REGISTRATION NUMBER: 36,203

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 120:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1442 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: both

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 15..1139

US-08-340-426D-120

Query Match 1.0%; Score 21; DB 2; Length 1442;

Best Local Similarity 100.0%; Pred No. 4.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1858 TAAAAAAATATAATAAAG 1878

DB 446 TAAAAAAATATAATAAAG 426

RESULT 9

US-08-450-673C-120/C

; Sequence 120; Application US/08450673C

; Patent No. 5948688

; GENERAL INFORMATION:

; APPLICANT: de la Monte, Suzanne

; APPLICANT: Wands, Jack R.

; TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection

TITLE OF INVENTION: of Alzheimer's Disease

NUMBER OF SEQUENCES: 121

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.

; STREET: 1100 New York Avenue, Suite 600

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/450,673C

; FILING DATE: 30-MAY-1995

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Ludwig, Steven R.

; REGISTRATION NUMBER: 36,203

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 371-2600

; TELEFAX: (202) 371-2540

; INFORMATION FOR SEQ ID NO: 120:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1442 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: both

; MOLECULE TYPE: CDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 15..1139

US-08-450-673C-120

Query Match 1.0%; Score 21; DB 2; Length 1442;

Best Local Similarity 100.0%; Pred No. 4.4;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1858 TAAAAAAATATAATAAAG 1878

DB 446 TAAAAAAATATAATAAAG 426

RESULT 10

US-08-594-031-154

; Sequence 154; Application US/08594031

; Patent No. 5783182

; GENERAL INFORMATION:

; APPLICANT: THOMPSON, Timothy C.

; TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES

; NUMBER OF SEQUENCES: 175

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BAKER & BOTT, L.L.P.

; STREET: 1299 Pennsylvania Avenue, N.W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004-2400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/594,031

; FILING DATE: 30-JAN-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/006,838

FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-594-031-154

Query Match 1.0%; Score 20; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

OY 1862 AAAATATAATATAAGAAA 1881
DB 260 AAAATATAATATAAGAAA 279

RESULT 11
US-08-450-065-1/c
Sequence 1, Application US/08450065
Patent No. 5798105
GENERAL INFORMATION:
APPLICANT: Schoenmakers, Johannes G
APPLICANT: Konings, Rudolph NH
APPLICANT: Moelans, Inge IMD
TITLE OF INVENTION: No. 5798105el protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
STREET: Smithkline Beecham Corporate Patents -US
STREET: UW2220, Po Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450.065
FILING DATE: 25-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/949645
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: B2992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5065
TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: PLASMODIUM
STRAIN: FALCIPARUM
IMMEDIATE SOURCE:
CLONE: 16K
US-08-450-065-1

Query Match 1.0%; Score 20; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

OY 1858 TAAAAAATAAATAAAAA 1877
DB 20 TAAAAAATAAATAAAAA 1

RESULT 12
US-08-450-595-1/c
Sequence 1, Application US/08450595
Patent No. 5798106
GENERAL INFORMATION:
APPLICANT: Schoenmakers, Johannes G
APPLICANT: Konings, Rudolph NH
APPLICANT: Moelans, Inge IMD
TITLE OF INVENTION: No. 5798106el protein
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Smithkline Beecham Corporate Patents -US
STREET: UW2220, Po Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450.595
FILING DATE: 25-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/949645
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Jervis, Herbert H.
REGISTRATION NUMBER: 31,171
REFERENCE/DOCKET NUMBER: B2992
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-270-5065
TELEFAX: 215-270-5090
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 634 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: PLASMODIUM
STRAIN: FALCIPARUM
IMMEDIATE SOURCE:
CLONE: 16K
US-08-450-595-1

Query Match 1.0%; Score 20; DB 1; Length 634;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1858 TAAAAAAATATAATAAAA 1877
DB 20 TAAAAAAATATAATAAAA 1

RESULT 13

US-08-676-967-3
Sequence 3, Application US/08676967
Patent No. 5747317
GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC896-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2733 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-676-967-3

Query Match 1.0%; Score 20; DB 1; Length 2733;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1321 AATGAGGGAAGTGT 1340
DB 1087 AATGAGGGAAGTGT 1106

RESULT 14

US-08-676-974-3
Sequence 3, Application US/08676974
Patent No. 5770422
GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA

COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,974
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC896-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2733 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-676-974-3

Query Match 1.0%; Score 20; DB 1; Length 2733;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1321 AATGAGGGAAGTGT 1340
DB 1087 AATGAGGGAAGTGT 1106

RESULT 15

US-09-098-487-3
Sequence 3, Application US/09098487
Patent No. 5917025
GENERAL INFORMATION:
APPLICANT: COLLINS, Kathleen
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,487
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UC896-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2733 base pairs
TYPE: nucleic acid
STRANDEDNESS: double

TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-098-487-3

Query Match 1.0%; Score 20; DB 2; Length 2733;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1321 AATGAAAGGAAACTGTTT 1340
|||||
DB 1087 AATGAAAGGAAACTGTTT 1106

Search completed: April 16, 2002, 18:12:29
Job time: 6004 sec